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Sequence 7, Appli
Sequence 10, Appli
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Sequence 12, Appli
Sequence 10, Appli
Sequence 11, Appli
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Sequence 12, Appli
Patent No. 5187153
Patent No. 5220013
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Patent No. 5223482
Patent No. 5187153
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                                                                October 18, 2002, 10:33:53; Search time 13 Seconds (without alignments) 319.412 Million cell updates/sec
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Patent No. 546
Patent No. 546
Patent No. 522
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948
1 ADRERSIHDFCLVSKVVGRC......ACMLRCFRQQENPPLPLGSK 170
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/cgn2_6/ptodata/1/iaa/6A_COMB.pep:*
/cgn2_6/ptodata/1/iaa/6B_COMB.pep:*
/cgn2_6/ptodata/1/iaa/PCTUS_COMB.pep:*
/cgn2_6/ptodata/1/iaa/PCTUS_COMB.pep:*
GenCore version 5.1.3
Copyright (c) 1993 - 2002 Compugen Ltd.
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US-09-013-896A-11
US-08-422-333-12
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Sequence 2 Sequence 2 Sequence 1 Sequence 1 Sequence 2 Sequence 3 Sequence 2 Sequence 2 Sequence 3 Sequence 2 Sequence 3 Sequence 3		252; 0;
ii ii	NG FOR SAME THE PROTEIN SEAS	1; Length -92; 0; Indels
US-07-844-297-1 US-08-026-145-2 US-08-676-125A-18 US-09-136-012A-18 US-08-208-24A-1 US-08-208-24A-25 US-09-414-878-1 US-09-414-878-1 US-09-421-097-25 US-09-421-097-25 US-09-421-097-25 US-09-421-097-25 US-08-854-782-2 US-08-854-782-	MENTS DNA CODIN RODUCING ACPEAK & N.W. A A 134	948; DB No. 3.1e matches
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33 2 2 2 2 2 2 2 2 2 2 2 2 2 2 2 2 2 2	ULT 1  GURGES-660A-7  atent No. 5731412  GENERAL INFORMATIONE,  APPLICANT: SHIMOURA,  APPLICANT: KAWAGUCHI,  APLICANT: KAWAGUCHI,  APLICANT: KITAMURA, NO  TITLE OF INVENTION: NO  TITLE OF INVENTION: NO  TITLE OF INVENTION: NO  TITLE OF INVENTION: NO  STREET: 2100 Pennsyl  CITY: Washington  STREET: 2100 Pennsyl  CITY: Washington  STREET: 2100 Pennsyl  COUNTRY: USA  ZIP. 2003  ZIPRE: DC  COUNTRY: USA  ZIPRE: DC  COUNTRY: USA  ZIPRE: ACCOMPORTER: IBM PC COMPORTER: IBM PC COMPORTER: IBM PC COMPORTER: PAPLICATION DATA  APPLICATION NUMBER: PILING DATE: 24-JUL-  PRIOR APPLICATION NUMBER:  FILING DATE: 24-JUL-  PRIOR APPLICATION NUMBER:  FILING DATE: 24-JUL-  ATORNEY/AGENT INFORMAT  NAME: KIT, GOTGON  REGISTRATION NUMBER:  FILING DATE: 24-JUL-  ATORNEY/AGENT INFORWAT  NAME: KIT, GOTGON  REGISTRATION FOR SEQ ID NO  SEQUENCE CHARACTERISTIC  SEQUENCE CHARACTERISTIC  SEGUENCE CHARACTERISTIC  SEG	Simi O;
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Matches 170;
                                      US-09-071-709-10
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28 ADRERSIHDFCLVSKVVGRCRASMPRWWYNVTDGSCQLFVYGGCDGNSNNYLTKEECLKK 87
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                                                                                                           RWYFDVERNSCNNFIYGGCRGNKNSYRSEEACMLRCFRQQENPPLPLGSK 170
                                                                                                                             RWYFDVERNSCNNFIYGGCRGNKNSYRSEEACMLRCFRQQENPPLPLGSK 170
                                                                                                                                                                                                                                      Sequence 7, Application US/08974196
Patent No. 5854396
GENERAL INFORMATION:
APPLICANT: KHAMAGUCHI, Toshiya
APPLICANT: KTAMMURA, Naomi
TITLE OF INVENTION: NOVEL PROTEIN, DNA CODING FOR SAME
TITLE OF INVENTION: AND METHOD OF PRODUCING THE PROTEIN
NUMBER OF SEQUENCES: 7
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                               SUGHRUE, MION, ZINN, MACPEAK & SEAS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PatentIn Release #1.0, Version #1.25
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Pred. No. 3.1e-92;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                2100 Pennsylvania Avenue, N.W
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APPLICATION NUMBER: 08/685,660
FILING DATE: 24-UUL-1996
FILING DATE: 24-UL-1996
FILING DATE: 24-UUL-1995
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SOFTWARE: PatentIn Release #1.0,
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/974,196
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy Disk
COMPUTER: IBM PC compatible
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 NAME: KIT, Gordon
REGISTRATION NUMBER: 30,764
REFERENCE/DOCKET NUMBER: 0-
TELECOMMUNICATION INFORMATION:
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amino acid
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Matches 170; Conservative
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                                                                                    APPLICANT: Tang, Y. Tom
APPLICANT: Lal, Preett.
APPLICANT: Colley, Neil C.
APPLICANT: Guegler, Karl J.
APPLICANT: Patterson, Chandra
TITLE OF INVENTION: HUMAN PROTEASE ASSOCIATED PROTEINS
NUMBER OF SEQUENCES: 12
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ADDRESSEE: STERNE, KESSLER, GOLDSTEIN & FOX P.L.L.C. STREET: 1100 NEW YORK AVE., NW, STE. 600
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TITLE OF INVENTION: TISSUE FACTOR PATHWAY INHIBITOR-3
NUMBER OF SEQUENCES: 31
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Word Perfect 6.1 for Windows/MS-DOS 6.2
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Score 948; DB 4;
Pred. No. 3.1e-92;
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                                                                                                                                                                                                                                         CORRESPONDENCE ADDRESS:
ADDRESSEE: INCYTE PHARMACEUTICALS, INC
STREET: 3174 PORTER DRIVE
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Sequence 10, Application US/09071709 Patent No. 6171790
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Patent No. 6262233
GENERAL INFORMATION:
APPLICANT: GENTZ, REINER
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ATTORNEY/AGENT INFORMATION:
NAME: CERRONE, MICHAEL C.
REGISTRATION NUMBER: 39,132
REFERENCE/DOCKET NUMBER: PF-0:
TELECOMMUNICATION INFORMATION:
TELEFRONE: (650) 855-055
TELEFRAX: (650) 845-416
INFORMATION FOR SEQ ID NO: 10:
                                                                    APPLICANT: Hillman, Jennifer L.
APPLICANT: Tang, Y. Tom
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MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
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                                          GENERAL INFORMATION:
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JPA Hei 7-187135

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FILING DATE: 24-JUL-1995
INFORMATION FOR SEQ ID NO: 18
SEQUENCE CHARACTERISTICS:
LENGTH: 513 anino acids
        APPLICATION NUMBER:
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US-08-685-558A-18
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1 ADRERSIHDFCLVSKVVGRCRASMPRWWYNVTDGSCQLFVYGGCDGNSNNYLTKEECLKK 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                28 ADRERSIHDFCLVSKVVGRCRASMPRWWYNVTDGSCQLFVYGGCDGNSNNYLTKEECLKK 87
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match 100.0%; Score 948; DB 4; Length 252; Best Local Similarity 100.0%; Pred. No. 3.1e-92; Matches 170; Conservative 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     RWYFDVERNSCNNFIYGGCRGNKNSYRSEEACMLRCFRQQENPPLPLGSK 170
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             148 RWYFDVERNSCNNFIYGGCRGNKNSYRSEEACMLRCFRQQENPPLPLGSK 197
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         APPLICANT: SHIMOMURA, Takeshi
APPLICANT: KHMMGUCHI, Toshiya
APPLICANT: KITANURA, Naomi
APPLICANT: KITANURA, Naomi
APPLICANT: KITANURA, Naomi
TITLE OF INVENTION: NOVEL PROTEIN, DNA CODING FOR SAME
TITLE OF INVENTION: AND METHOD OF PRODUCING THE PROTEIN
NUMBER OF SEQUENCES: 18
CORRESPONDENCESS:
ADDRESSEE: SUGHRUE, MION, ZINN, MACPEAK & SEAS
                                                                             COMPUTER READBALE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              E: SUGHRUE, MION, ZINN, MACPEAK & SEAS 2100 Pennsylvania Avenue, N.W.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SOFTWARE: Patentin Release #1.0, Version #1.25 CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                    1488.1290001
                                                                                                                                                                                                            APPLICATION NUMBER: US/09/013,896A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               APPLICATION NUMBER: US/08/685,558A FILING DATE: 24-JUL-1996 PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          MEDIUM TYPE: Floppy Disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence 18, Application US/08685558A Patent No. 6225081
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                 ATTORNEY AGENT INFORMATION:
NAME: STEFFE, ERIC K.
REGISTATION NUMBER: 36,688
REFERENCE/DOCKET NUMBER: 1488.
TELECOMMUNICATION INFORMATION:
TELEFAX: (301) 309-8504
TELEFAX: (301) 309-8439
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                              : 252 amino acids
amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TOPOLOGY: linear

MOLECULE TYPE: protein

US-09-013-896A-2
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COMPUTER READABLE FORM:
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CLASSIFICATION: 435
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      WASHINGTON
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US-08-685-558A-18
CITY: WASTATE: D
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244 KQTEDYCLASNKVGRCRGSFPRWYDPTEQICKSFVYGGCLGNKNNYLREEECILACRGV 303
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     EE----YCTANAVTGPCRASFPRWYFDVERNSCNNFIYGGCRGNKNSYRSEEACML 154
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    5 RSIHDFCLVSKVVGRCRASMPRWWYNVTDGSCQLFVYGGCDGNSNNYLTKEECLKKCATV 64
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              304 QGPSMERRHPVCSGTCQPTQFRCSNGCCIDSFLECDDTPNCPDASDEAACEKYTSGFDEL
                                                                                                                                                                                                                            32.9%; Score 312; DB 4; Length 513; 33.5%; Pred. No. 7.6e-25; ive 24; Mismatches 71; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence 2, Application US/09071709
Patent No. 6171790
GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT: Tang, Y. Tom
APPLICANT: Lal, Preeti
APPLICANT: Corley, Neil
APPLICANT: Corley, Neil
APPLICANT: Corley, Neil J.
APPLICANT: Patterson, Chandra
TITLE OF INVENTION: HUMAN PROTEASE ASSOCIATED PROTEINS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Word Perfect 6.1 for Windows/MS-DOS 6.2
CURRENT APPLICATION DATA: US/09/071,709
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CORRESPONDENCE ADDRESS:
ADDRESSEE: INCYTE PHARMACEUTICALS, INC.
STREET: 3174 PORTER DRIVE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ATTORNEY/AGENT INFORMATION:
NAME: CERRONE, MICHAEL C.
REGISTRATION NUMBER: 39,132
REFERENCE/DOCKET NUMBER: PF-0513 US
TELECOMMUNICATION INFORMATION:
TELEPHONE: (650) 855-0555
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Filed Herewith
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INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
                                            TOPOLOGY: linear
MOLECULE TYPE: peptide
ORIGINAL SOURCE:
ORGANISM: Homo sapiens
                                                                                                                                                                                                                                                                                 67; Conservative
                            single
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STREET: 31/4 CLTO
CLTY: CALLFORNIA
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TYPE: amino acid
STRANDEDNESS: si
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us-09-218-913d-52.rai

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Matches
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                                                                                                                                                                                                                                                                                                           122 V----QGGPLRGSSGAQATFPQGPSMERRHPVCSGTCQPTQFRCSNGCCIDSFLECDDTP 177
                                                                                                                                                                                                                                                                                                                                                                                                                                                         95 ---HSSDMFNYEEY-------CTANAVTGPCRASFPRWYFDVERNSCNN 133
                                                                                                                                                                                                                                                                                5 RSIHDFCLVSKVVG-RCRASMPRWWYNVTDGSCQLFVYGGCDGNSNNYLTKEECLKKCAT 63
                                                                                                                                                                                                                                                                                                                                                                        --DSED-- 94
                                                                                                                                                                                                 Length 348;
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Sequence 10, Application US/09013896A
Fatent No. 626233
GENERAL INFORMATION:
APPLICANT: GENTZ, REINER
TITLE OF INVENTION: TISSUE FACTOR PATHWAY INHIBITOR-3
NUMBER OF SEQUENCES: 31
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ADDRESSEE: STERNE, KESSLER, GOLDSTEIN & FOX P.L.L.C.
STREET: 1100 NEW YORK AVE., NW, STE. 600
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  COMPUTER: LEMP PC compatible
COMPUTER: IBM PC compatible
COMPUTER: IBM PC compatible
COMPUTER: IBM PC compatible
CONTAME: Patentin Release #1.0, Version #1.30
CURREWT APPLICATION DATA:
APPLICATION NUMBER: US/09/013,896A
FILING DATE:
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: STREEF, ERIC K.
REGISTRATION NUMBER: 1488.1290001
TELEPATION NUMBER: 1488.1290001
TELEPATION INFORMATION:
TELEPATION INFORMATION:
TELEPAX: (301) 309-8439
INFORMATION FOR SEQ ID NO: 10:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   134 FIYGGCRGNKNSYRSEEACMLRC-----FRQQENPPLP 166
                                                                                                                                                                                                 DB 4;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match 31.3%; Score 297; DB 4; Best Local Similarity 100.0%; Pred. No. 1.5e-24; Matches 51; Conservative 0; Mismatches 0;
                                                                                                                                                                                             31.6%; Score 299.5; DB 4 ilarity 31.2%; Pred. No. 9.6e-24; Conservative 24; Mismatches 65
                                                                                                                                                                                                                                                                                                                                                                      64 VTENATGDLATSRNAADSSVPSAP---RRQ--
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LENGTH: 348 amino acids
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                    TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ZIP: 20005
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TOPOLOGY: linear MOLECULE TYPE: protein
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                                                                                 ; IMMEDIATE SOURCE:
; LIBRARY: BLADNOT04
; CLONE: 1319265
US-09-071-709-2
                                                                                                                                                                                             Query Match
Best Local Similarity
Matches 69; Conserva
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CITY: WASHINGTON STATE: DC
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APPLICANT: CORDELL, BATDARA L.
TITLE OF INVENTION: TRANSCENIC NON-HUMAN MAMMAL DISPLAYING
TITLE OF INVENTION: THE AMYLOID-FORMING PATHOLOGY OF ALZHEIMER'S DISEASE
NUMBER OF SEQUENCES: 30
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           106 CTANAVTGPCRASFPRWYFDVERNSCNNF1YGGCRGNKNSYRSEEACMLRC 156
61
                                       51
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                        1 CLVSKVVGRCRASMPRWWYNVTDGSCQLFVYGGCDGNSNNYLTKEECLKKC
11 CLVSKVVGRCRASMPRWWYNVTDGSCQLFVYGGCDGNSNNYLTKEECLKKC
                                                                                                                                                                                 GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT: GENTZ, REINER
TITLE OF INVENTION: TISSUE FACTOR PATHWAY INHIBITOR-3
NUMBER OF SEQUENCES: 31
CORRESPONDENCE ADDRESS:
ADDRESSE: STERNE, KESSLER, GOLDSTEIN & FOX P.L.L.C.
STREET: 1100 NEW YORK AVE., NW, STE. 600
CITY: WASHINGTON
                                                                                                                                                                                                                                                                                                                                                                                                                   COMPUTER READABLE FORM:
MEDIUM TYPE: PLOPPY disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/013,896A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Score 297; DB 4; I
Pred. No. 1.5e-24;
0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1488.1290001
                                                                                                                        US-09-013-896A-11; Sequence 11, Application US/09013896A; Patent No. 6262233
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   US-08-422-333-12; Sequence 12, Application US/084223333; Patent No. 5912410
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100.0%; Prf
0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ATTORNEY/AGENT INFORMATION:
NAME: STEFFE, ERIC K.
REGISTRATION NUMBER: 36,688
REFRENCE/DOCKET NUMBER: 1488.
TELECOMMUNICATION INFORMATION:
TELEPHONE: (301) 309-8504
TELEFAX: (301) 309-8504
ILEPRAX: (301) 309-8504
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              E: Scios, Inc.
2450 Bayshore Parkway
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ZIP: 94043
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           51 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 51; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        MOLECULE TYPE: protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CLASSIFICATION: 435
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Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                US-09-013-896A-11
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69 TGDLATSRNAADSSVPSAPRRQDSEDHSSDMFNYEEYCTANAVTGPCRASFPRWYFDVER 128
                                                                                                                    129 NSCNNFIYGGCRGNKNSYRSEEACMLRC 156
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             84 GKCVRFSYGGCKGNGNKFYSQKECKEYC 111
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       E: Scios, Inc.
2450 Bayshore Parkway
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                E: Floppy disk
IBM PC compatible
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 FILING DATE: 31-DEC-1986
APPLICATION NUMBER: 932,193
FILING DATE: 17-NOV-1986
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Mountain View
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        OPERATING SYSTEM:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match
Best Local Similarity
Matches 48; Conserv
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5220013-23
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          STREET:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SEQ ID NO:23
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                               9 DFCLVSKVVGRCRASMPRWWYNVTDGSCQLFVYGGCDGNSNNYLTKEECLKKCATVTENA 68
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      RESULT 10
5187153-20
; PATON NO. 5187153
APPLICANT: CORDELL, BARBARA; SCHILLING, JAMES W.; KATUNUMA, NOBUHIKO; TITLE OF INVENTION: METHODS OF TREATMENT USING ALZHEIMER'S; MAYLOID POLYPEPTIDE DERIVATIVES
NUMBER OF SEQUENCES: 333
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                3 DSCQLDYSQGPCLGLFKRYFYNGTSMACETFLYGGCMGNLNNFLSQKECLQTCRTV---
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                                                                                                                                                                                                                                                                                                                                                                                                            Length 122;
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                                    PatentIn Release #1.0, Version #1.30
                                                                                                                                                                                                                                                                                                                                                                                                            DB 2;
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                                                                                                                                                                                                                                                                                                                                                                                                      Query Match 26.1%; Score 247.5; DB 2
Best Local Similarity 32.4%; Pred. No. 7.5e-19;
Matches 48; Conservative 16; Mismatches 45
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Score 247.5; DB 6
Pred. No. 7.5e-19;
                                                                              FILING DATE: 13-ARR-1995
CLASSIFICATION: 800
ATTORNEY/AGENT INFORMATION:
NAME: Shearer, Peter R.
REGISTRATION NUMBER: 28,117
REFERENCE/DOCKET NUMBER: 21900-28048.00
TELECHOMONICATION INFORMATION:
TELEPHONE: (415) 966-1550
TELEFAX: (415) 968-2438
INFORMATION FOR SEQ ID NO: 12:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 16; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CURRENT ACTUALINGS

APPLICATION DATA

APPLICATION NUMBER: US/07/502,273

FILING DATE: 29-MAR-1990

PRIOR APPLICATION DATA:

APPLICATION NUMBER: 361,912

FILING DATE: 06-JUN-1989

APPLICATION NUMBER: 359,911

FILING DATE: 12-MAY-1989

APPLICATION NUMBER: 87,002

FILING DATE: 18-MG-1987

APPLICATION NUMBER: 8,810

FILING DATE: 30-JAN-1987

APPLICATION NUMBER: 9,810
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                                               CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/422,333
FILING DATE: 13-APR-1995
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              26.1%;
32.4%;
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APPLICATION NUMBER: 932,1
FILING DATE: 17-NOV-1986
                                                                                                                                                                                                                                                                                             122 amino acids
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Best Local Similarity 32.49
Matches 48; Conservative
                                                                                                                                                                                                                                                                                                                                     single
                                                                                                                                                                                                                                                                                                                TYPE: amino acid
STRANDEDNESS: si
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5187153-20
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APPLICANT: CORBELL, BATBARA L.
APPLICANT: CORBELL, BATBARA L.
TITLE OF INVENTION: TRANSGENIC NON-HUMAN MAMMAL DISPLAYING
TITLE OF INVENTION: TRANSCENIC NON-HUMAN MAMMAL DISPLAYING
TITLE OF INVENTION: THE AMYLOID-FORMING PATHOLOGY OF ALZHBIMER'S DISEASE
NUMBER OF SEQUENCES: 30
CORRESPONDENCE ADDRESS:
ADDRESSEE: SCIOS, INC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   69 TGDLATSRNAADSSVPSAPRRQDSEDHSSDMFNYEEYCTANAVTGPCRASFPRWYFDVER 128
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------EACNLPIVOGPCRAFIQLWAFDAVK 83
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           9 DFCLVSKVVGRCRASMPRWWYNVTDGSCQLFVYGGCDGNSNNYLTKEECLKKCATVTENA 68
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                                                                                                                                                                                                                                                    Patent No. 5220013

Patent No. 5220013

TITLE OF INVENTION: DNA SEQUENCE USEFUL FOR THE DETECTION

OF ALZHEIMER'S DISEASE

NUMBER OF SEQUENCES: 30

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/07/444,118

FILING DATE: 30-NOV-1989

PRIOR APPLICATION DATA:

APPLICATION NUMBER: 8,810

FILING DATE: 18-AUG-1987

APPLICATION NUMBER: 8,810

FILING DATE: 30-JAN-1987

APPLICATION NUMBER: 9,48,376
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Length 122;
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SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DARA:
APPLICATION NUMBER: US/08/422,333
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 26.1%; Score 247.5; DB 6; 32.4%; Pred. No. 7.5e-19; ive 16; Mismatches 45;
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69 IGDLATSRNAADSSVPSAPRRQDSEDHSSDMFNYEEYCTANAVTGPCRASFPRWYFDVER 128
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TITLE OF INVENTION: DOMAINS THAT INHIBIT HUMAN NEUTROPHIL ELASTASE
                                                                                                                                          Patent No. 5187153

**Patent No. 5187153

**Patent No. 5187153

**TILLE OF INVENTION: METHODS OF TREATMENT USING ALZHEIMER'S TILLE OF INVENTION: METHODS OF TREATMENT USING ALZHEIMER'S CURRENT APPLICATION DATE: DEPLICATION NUMBER: US/07/502,273

**PLICATION NUMBER: US/07/502,273

**PLICATION NUMBER: 359,911

**PLICATION NUMBER: 359,911

**PLICATION NUMBER: 87,002

**PLICATION NUMBER: 87,002
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Length 144;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Score 244.5;
Pred. No. 1.9
  105 GKCVLFPYGGCQGNGNKFYSEKECREYC 132
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       129 NSCNNFIYGGCRGNKNSYRSEEACMLRC 156
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STREET: 419 Seventh Street, N.W.
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COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence 72, Application US/08358160 Patent No. 5663143
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            GENERAL INFORMATION:
APPLICANT: LEY, Arthur C.
APPLICANT: LADNER, Robert C.
APPLICANT: GUTERMAN, Sonia K.
APPLICANT: ROBERTS, Bruce L.
APPLICANT: MARKLAND, William
APPLICANT: KENT, Rechel B.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        25.8%; Scoilarity 31.8%; Pro
Conservative 15;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              FILING DATE: 31-DEC-1986
APPLICATION NUMBER: 932,193
FILING DATE: 17-NOV-1986
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          APPLICATION NUMBER: 948,376
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CITY: Washington
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match
Best Local Similarity
Matches 47; Conserv
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                                                                                                 RESULT 14
5187153-18
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      9 DFCLVSKVVGRCRASMPRWWYNVTDGSCQLFVYGGCDGNSNNYLTKEECLKKCATVTENA 68
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              9 DFCLVSKVVGRCRASMPRWWINVTDGSCQLFVYGGCDGNSNNYLTKEECLKKCATVTENA 68
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                        39:
                                                                                                                                                                                                                                                                                                                                                                                                                          Length 143;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     APPLICANT: SCHILLING, JAMES W.; PONTE, PHYLLIS A.; CORDELL,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TITLE OF INVENTION: RECOMBINANT ALZHEIMER'S PROTEASE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Score 244.5; DB 6;
Pred. No. 1.9e-18;
                                                                                                                                                                                                                                                                                                                                                                                                                       DB 2;
                                                                                                                                                                                                                                                                                                                                                                                                                       s; Score 244.5; DB 2b; Pred. No. 1.9e-18;15; Mismatches 47
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NUMBER OF SEQUENCES: 34

CURRENT APPLICATION DATA:

APPLICATION DATA:

FILING DATE: 06-JUN-1989

FRIOR APPLICATION DATA:

APPLICATION NUMBER: 359,911

FILING DATE: 12-MAY-1989

APPLICATION NUMBER: 87,002

FILING DATE: 18-AUG-1987

APPLICATION NUMBER: 8,810

FILING DATE: 13-MAY-1987

APPLICATION NUMBER: 8,810

FILING DATE: 30-JAN-1987

APPLICATION NUMBER: 948,376

FILING DATE: 31-DEC-1986
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                                                                                                                        21900-28048.00
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                 CLASSIFICATION: 800
ATTORNEY AGENT INFORMATION:
NAME: Shearer, Peter R. REGISTRATION NUMBER: 28,117
REFERENCE/DOCKET NUMBER: 2190
TELECOMMUNICATION: TELECHONE: (415) 966-150
TELEFAX: (415) 966-150
INFORMATION FOR SEQ ID NO: 10: SEGUENCE CHARATERISTICS:
LENGTH: 143 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             APPLICATION NUMBER: 932,193
FILING DATE: 17-NOV-1986
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                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match 25.8%;
Best Local Similarity 31.8%;
Matches 47; Conservative 1
13-APR-1995
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Best Local Similarity 31.8%
Matches 47; Conservative
                                                                                                                                                                                                                                                                                                                         single
                                                                                                                                                                                                                                                                                            TYPE: amino acid
STRANDEDNESS: Si
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US-08-422-333-10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SEQ ID NO:20
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Ouery Match 25.8%; Score 244.5; DB 1; Length 147; Best Local Similarity 32.4%; Pred. No. 2e-18; Matches 48; Conservative 14; Mismatches 47; Indels 39;
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/358,160
FILING DATE: 16-DEC-1994
                                                                                     FILING DATE: 10-DEC 10-DEC CLASSIFICATION: 514

PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/133,031
FILING DATE: 13-OCT-1993
PRIOR APPLICATION NUMBER: US 08/009,319
FILING DATE: 26-JAN-1993
PRIOR APPLICATION NUMBER: US 07/664,989
FILING DATE: 01-MAR-1991
PRIOR APPLICATION NUMBER: US 07/664,989
FILING DATE: 01-MAR-1990
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/240,160
FILING DATE: 02-MAR-1990
PRIOR APPLICATION NUMBER: US 07/240,160
FILING DATE: 02-MAR-1990
ATTORNEY,AGENT INFORMATION:
NAME: COOPER, IVER P.
REGISTRATION NUMBER: 28,005
REFERENCE/DOCKET NUMBER: LEY-1
TELECOMMUNICATION INFORMATION:
TELEPHONE: 202-628-5197
TELECOMMUNICATION INFORMATION:
TELEPHONE: 202-637-3528
TELEEX: 248633
INFORMATION FOR SEQ ID NO: 72:
LENGTH: 147 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: protein
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69 TGDLATSRNAADSSVPSAPRRQDSEDHSSDMFNYEEYCTANAVTGPCRASFPRWYFDVER 128 δy ò

qq

Gaps

47; Indels 39;

129 NSCNNFIYGGCRGNKNSYRSEEACMLRC 156

105 GKCVLFPYGGCQGNGNKFYSEKECREYC 132

Search completed: October 18, 2002, 10:36:06 Job time: 15 secs

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GenCore version 5.1.3 Copyright (c) 1993 - 2002 Compugen Ltd.

OM protein - protein search, using sw model

October 18, 2002, 10:33:48 ; Search time 28 Seconds (without alignments) 1050.326 Million cell updates/sec Run on:

US-09-218-913D-52 948 1 ADRERSIHDFCLVSKVVGRC......ACMLRCFRQQENPFLPLGSK 170 Title: Perfect score: Sequence:

BLOSUM62 Gapop 10.0 , Gapext 0.5 Scoring table:

562222 seqs, 172994929 residues Searched:

Minimum DB seq length: 0 Maximum DB seq length: 200000000

Total number of hits satisfying chosen parameters:

562222

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

Database :

sp\_fungi:\*
sp\_human:\*
sp\_invertebrate:\*
sp\_mammal:\* sp\_archea:\* sp\_bacteria:\* SPTREMBL\_19:\* sp\_mhc:\*

sp\_unclassified:\*
sp\_rvirus:\*
sp\_bacteriap:\*
sp\_archeap:\* sp\_virus:\*
sp\_vertebrate:\* sp\_organelle:\* sp\_phage:\* sp\_plant:\* sp\_rodent:\*

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Description •	Q969e0 homo sapien	Q9d8q8 mus musculu	Q9d3k4 mus musculu	099104 mus musculu	O9vav4 drosophila	044938 haemonchus	Q9u8q8 manduca sex	093424 cyprinus ca	076840 caenorhabdi	Q9qqr0 drosophila	P78491 homo sapien	045881 caenorhabdi	Q28874 canis famil	Ogdbig mus musculu	0925w1 mus musculu	O70160 cavia porce .
ID	Q969E0	090808	Q9D3K4	099304	<b>09VAV4</b>	044938	Q9U8G8	093424	076840	Q9GQR0	P78491	045881	028874	Q9DBJ9	Q925W1	070160
DB	4	11	11	11	ស	Ŋ	വ	13	വ	ហ	4	Ŋ	ڡ	11	11	11
% Query Match Length DB	252	195	507	507	3060	1572	3198	287	2167	2174	151	2225	396	349	349	352
& Query Match	100.0	40.2	31.0	31.0	27.3	27.1	26.9	26.6	26.4	26.4	25.8	25.3	25.3	24.8	24.8	24.6
Score	948	381	294	294	259	256.5	255	252	250.5	250	244.5	240	239.5	235.5	235.5	233.5
Result No.		2	m	4	2	9	7	8	6	10	11	12	13	14	15	16

O95103 homo sapien Q92208 mus musculu O17644 caenorhabdi	P70004 xenopus lae Q21418 caenorhabdi		Q60709 mus musculu O61482 mus musculu	homo		Q22685 caenorhabdi			Q9u350 caenorhabdi	062504 caenorhabdi	Q96s20 homo sapien		Q9dgj7 gallus gall		O	Q99qn1 calliactis	homo	homo	sns	045916 caenorhabdi	Q99k32 mus musculu	Q9qz78 cavia sp. p		09twf8 anemonia su
095103 Q9Z2U8 O17644	P70004 Q21418	O9XWX5	060709	014594	009983	022685	Q9N343	019021	090350	062504	096820	096NZ8	Q9DGJ7	091963	Q9GQN2	Q9GQN1	013793	013764	OINT60	045916	Q99K32	090Z78	061893	Q9TWF8
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251 246 1043	342 922	1743	751	523	1599	1522	1195	1391	1297	1474	491	548	751	747	984	984	484	547	770	1203	607	160	1965	59
24.1 24.0 23.4	23.2	22.0	21.9	21.1	21.1	21.0	20.9	20.6	20.5	20.4	20.3	20.3	19.8	19.7	19.7	19.7	19.6	19.6	19.6	19.6	19.4	19.3	18.8	18.7
228 227.5 222	219.5 219	209	208	200	200	199	198	195	194	193	192	192	188	186.5	186.5	186.5	186	186	186	185.5	183.5	æ	178	177
17 18 19	20	22	23	25	56	27	28	53	30	31	32	33	34	35	36	37	38	39	40	41	42	43	44	45

## ALIGNMENTS

	IMINARY; PRT; 252 AA.			MBLrel. 19, Last annotation update)	SERINE PROTEASE INHIBITOR, KUNITZ TYPE, 2.	nan).	oa; Chordata; Craniata; Vertebrata; Euteleostomi;	la; Primates; Catarrhini; Hominidae; Homo.		ı.i.	) ADENOCARCINOMA;		Submitted (AUG-2001) to the EMBL/GenBank/DDBJ databases.	ښد	) ADENOCARCINOMA;	Strausberg R.;	101) to the EMBL/GenBank/DDBJ databases.	· i	) ADENOCARCINOMA;		101) to the EMBL/GenBank/DDBJ databases.	AAH12868.1;	AAH07705.1;	AAH11951.1;	AAH11955.1;		1; 28242 MW; FDD3360C1F3A7057 CRC64;		TOU.U%; SCOIE 948; DB 4; LENGIN 232; -v 100 0%: Dred No 8 3e-93:	vative 0;
	PRELIMINARY;	19,	19,	(TrEMBLrel. 19, L	ASE INHIBITOR, KU	(Human).	etazoa; Chordata;	theria; Primates;	606;	M N.A.	TISSUE=OVARY, AND ADENOCARCINOMA;	•	UG-2001) to the E	M N.A.	TISSUE=OVARY, AND ADENOCARCINOMA;	::	AY-2001) to the E	M N.A.	TISSUE=OVARY, AND ADENOCARCINOMA;	Strausberg R.;	UL-2001) to the E				55; AAH11955.1; -		252 AA; 28242 MW;	000		vative
RESULT 1	ID 0969E0	DT 01-DEC-2001	DT 01-DEC-2001	_		OS Homo sapiens (Human)	OC Eukaryota; Metazoa;		OX NCBI_TaxID=9606;			RA Strausberg R	RL Submitted (A	RP SEQUENCE FROM N.A.		RA Strausberg R	RL Submitted (M.					EMBL;	EMBL;	EMBL;	DR EMBL; BC011955;	KW Protease.	SEQUENCE	40.40%	Query Match Best Local Similarity	Matches 170;

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1 ADRERSIHDFCLVSKVVGRCRASMPRWWYNVTDGSCQLFVYGGCDGNSNNYLTKEECLKK 60

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SC 419
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                                                                                                                              SPINT1.
                                                       Q9D3K4;
                                         09D3K4
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                RESULT 3
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                                                          64 VTENATGDLATSRNAADSSVPSAPRRQDSEDHSSDMFNYEEYCTANAVTGPCRASFPRWY 123
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Gaps
             87
             ADRERSIHDFCLVSKVVGRCRASMPRWWYNVTDGSCOLFVYGGCDGNSNNYLTKEECLKK
                                         CATVTENATGDLATSRNAADSSVPSAPRRODSEDHSSDMFNYEEYCTANAVTGPCRASFP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 "Functional annotation of a full-length mouse cDNA collection."; Nature 409:685-690(2001).
EMBL; AK007792; BAB25258.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match
40.2%; Score 381; DB 11; Length 195;
Best Local Similarity 64.5%; Pred. No. 1.1e-32;
Matches 69; Conservative 14; Mismatches 24; Indels
                                                                                               RWYFDVERNSCNNFIYGGCRGNKNSYRSEEACMLRCFRQQENPPLPLGSK 170
                                                                                                              148 RWYFDVERNSCNNFIYGGCRGNKNSYRSEBACMLRCFRQQENPPLPLGGK 197
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             FDVERNSCNNFIYGGCRGNKNSYRSEEACMLRCFRQQENPPLPLGSK 170
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       21705 MW; 1ABD78CEF1175DE1 CRC64;
                                                                                                                                                                                                                                         01.JUN-2001 (TrEMBLrel. 17, Last sequence update) 01-DEC-2001 (TrEMBLrel. 19, Last annotation update) SERINE PROTEASE INHIBITOR, KUNITZ TYPE 2.
                                                                                                                                                                                                                           (TrEMBLrel. 17, Created)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PROSITE; PS00280; BPTI_KUNITZ_1; 1. PROSITE; PS50279; BPTI_KUNITZ_2; 1. Serine protease inhibitor.
                                                                                                                                                                                                  PRT;
                                                                                                                                                                                                                                                                                                                                                                               STRAIN-C57BL/6J; TISSUE-PANCREAS; MEDLINE-21085660; Pubmed-11217851;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    InterPro; IPR002223; Kunitz_BPTI
                                                                                                                                                                                                                        01-JUN-2001 (TrEMBLrel. 17, 01-JUN-2001 (TrEMBLrel. 17, 01-DEC-2001 (TrEMBLrel. 19,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Pfam; PF00014; Kunitz_BPTI; PRINTS; PR00759; BASICPTASE.
SMART; SM00131; KU; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Spint2
                                                                                                                                                                                                PRELIMINARY;
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                                                                                                                                                                                                                                                                                                                                                                     SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                       NCBI_TaxID=10090;
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                                                                                                                                                                                                                                                                                                Mus musculus
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             28
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RA Arakwa T., Hara A., Shibata K., Yoshino M., Itoh M., Ishii Y.,
Rawai J., Shinagawa A., Shibata K., Yoshino M., Itoh M., Ishii Y.,
Arakwa T., Hara A., Fukunishi Y., Konoo H., Adachi J., Fukuda S.,
RA Ataawa K., Izawa M., Nishi K., Kiyosawa H., Kondo S., Yamanaka I.,
RA Saito T., Okazaki Y., Gojobori T., Bono H., Kasukawa T., Saito R.,
RA Gadota K., Matsuda H.A., Ashburner M., Batalov S., Casvant T.,
RA Fleischmann W., Gaasterland T., Gissi C., King B., Kochiwa H.,
RA Kuehl P., Lewis S., Matsuo Y., Nikaido I., Pesole G., Quackenbush J.,
RA Schriml L.M., Staubli F., Suzuki R., Tomita M., Wagner L., Washio T.,
RA Brownstein M.J., Bult C., Fletcher C., Fujita M., Gariboldi M.,
RA Brownstein M.J., Bult C., Fletcher C., Fujita M., Gariboldi M.,
RA Brownstein M.J., Hofmann M., Hume D.A., Kamiya M., Lee N.H.,
RA Mordone P., Ring B., Ringwald M., Rodriguez I., Saamanco N.,
A Nordone P., Ring B., Ringwald M., Rodriguez I., Saamanco N.,
Sasaki H., Sato K., Schoenbach C., Seya T., Shibata Y., Storch K.-F.,
RA Winshaw-Boris A., Yoshida K., Haseqawa Y., Kawaji H., Kohtsuki S.,
A Wanshar-Boris A., Yoshida K., Haseqawa Y., Kawaji H., Kohtsuki S.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              38 KQTEDYCLASYKVGRCRGSFPRWYYDPKEQICKSFTFGGCLGNKNNYLREEGCMLACKDV 297
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Gaps
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                                                                                                                                                                                                                                                                       Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Musinae; Mus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                298 QGISPKRHHPVCSGSCHATQFRCSNGCCIDGFLECDDTPDCPDGSDEATCEKYTSGFDEL
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        'Functional annotation of a full-length mouse cDNA collection.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          30;
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7 AA; 56571 MW; 9EE0A29B7056D72D CRC64;
                                                                                                       Last sequence update)
Last annotation update)
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; Pred. No. 5.8e-23;
23; Mismatches 70;
507 AA
                                                                                                                                                                       SERINE PROTEASE INHIBITOR, KUNITZ TYPE 1
                                                                          Created)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PROSITE; PS00280; BPTI_KUNITZ_1; 1. PROSITE; PS50279; BPTI_KUNITZ_2; 2. PROSITE; PS50068; LDLRA_2; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                              STRAIN=C57BL/6J; TISSUE=HEAD;
MEDLINE=21085660; PubMed=11217851;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    MGD; MGI:1338033; Spintl.
InterPro; IPR002223; Kunitz_BPTI.
InterPro; IPR002172; LDL_recept_A
Pfam: PF00014; Kunitz_BPTI; 2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Pfam; PF00057; ldl_recept_a; l.
PRINTS; PR00759; BASICPTASE.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Nature 409:685-690(2001).
EMBL; AK017342; BAB30697.1; -.
HSSP; P05067; 1CA0.
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32.4%;
                                                                       (TrEMBLrel, 17,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Best Local Similarity 32.49
Matches 59; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SMART; SM00192; LDLa; 1.
                                                                                                   (TrEMBLrel.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SMART; SM00131; KU; 2.
                                                                                                                                                                                                                                       (Mouse)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Glycoprotein; Serin
SEQUENCE 507 AA;
                                                                                                                                                                                                                                                                                                                                                                                                              SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                              NCBI_TaxID=10090;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Hayashizaki Y.;
                                                                                                                                                                                                                                   Mus musculus
                                                                   01-JUN-2001
                                                                                                   01-JUN-2001
01-DEC-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            RC 156
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PROSITE;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  VARSPLIC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     VARSPLIC
3;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   O'9VAV4; OgVAV3;
O'9VAV4; OgVAV3;
O'STANTANON (TEMBLE) 13, Created)
O1-MAY-2000 (TEMBLE) 16, Last sequence update)
O1-MAR-2001 (TEMBLE) 19, Last annotation update)
CG1540 PROTEIN.
PRO CG1540 OR CG18436.
Drosophila melanogaster (Fruit fly).
BUKATYOCH; Merazoa; Arthropoda; Tracheata; Hexapoda; Insecta;
PHENYQCH2; Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
Ephydroidea; Drosophilidae; Drosophila.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              417
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         64
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             298 QGISPKRHHPVCSGSCHATQFRCSNGCCIDGFLECDDTPDCPDGSDEATCEKYTSGFDEL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       -----YCTANAVTGPCRASFPRWYFDVERNSCNNFIYGGCRGNKNSYRSEEACML
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               RSIHDFCLVSKVVGRCRASMPRWWYNVTDGSCQLFVYGGCDGNSNNYLTKEECLKKCATV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                -----TENATGDLATSRNAAD----SSVPSAPRRQDSEDHSSDMFNYEE-
                                                                                                                                                                                                                      Craniata; Vertebrata; Euteleostomi;
Sciurognathi; Muridae; Murinae; Mus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     30;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Length 507;
                                                                                                                                                                                                                                                                                                         Strausberg R.;
Submitted (APR-2001) to the EMBL/GenBank/DDBJ databases.
Submitted (APR-2001) to the EMBL/GenBank/DDBJ databases.
EMBL; BC005769; AAH05769.1;
HSSP; P05067; 10200.
MGD; MGI:1338033; Spint1.
InterPro; IPR002172; LDL_recept_A.
Pfam; PF00014; Kunitz_BPTI.
Pfam; PF00057; ldl_recept_a: 1.
PRINTS; PR00759; BASICPTASE.
SMART; SM00192; LDLa: 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Serine protease inhibitor.
                                                                                                                        01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
SERINE PROTEASE INHIBITOR, KUNITZ TYPE 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 31.0%; Score 294; DB 11; 32.4%; Pred. No. 5.8e-23; ive 23; Mismatches 70;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PRT; 3060 AA.
                                                                       202
                                                                                                         Created)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PROSITE; PS00280; BPTI_KUNITZ_1; 2. PROSITE; PS50279; BPTI_KUNITZ_2; 2. PROSITE; PS01209; LDLRA_1; 1. PROSITE; PS50068; LDLRA_2; 1. Glycoprotein; Protease; Serine prot SEQUENCE 507 AA; 56590 MW; F7F9
                                                                       PRT;
                                                                                                                                                                                                 Mus musculus (Mouse).
Eukaryota; Metazoa; Chordata;
Mammalia; Eutheria; Rodentia;
                                                                                                         (TrEMBLrel. 17,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PRELIMINARY;
                                                                       PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Local Similarity
les 59; Conserv
                                                                                                                                                                                                                                                                                            SEQUENCE FROM N.A.
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                                                                                                                                                                                                                                                           NCBI_TaxID=10090;
                                                                                                         01-JUN-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                RC 156
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                                                                       Q99J04
Q99J04;
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                                                                                                                                                                                  SPINT1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            238
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Q9VAV4
                                  RESULT 4
                                                   099704
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Michael Manuschiele, Publied-1071131;

Righting Continued Co. Scherer S. E. 11 P. W. Hosbits R. A. Galla B. R. F.,

Adman W. Goldening Co., Scherer S. E., 11 P. W. Hosbits R. A. Galla B. R. F.,

Rocerge R. A., Leafus S. E., Richards S., Ashburner M., Bedderson S. N.,

Brandon G. G., Worthan J. R., Xandell M. D., Zhang O., Chen L. N.,

Brandon C. C., Barder S. F., Richards R. C., Change M. P. Feiffer B. D.,

A brill J. F. Apbayan, A. An H. J. Andrews-Frankoch C., Baldain D.,

Brandon R. W., Basa A., Dastella S., Bayhatrargul Loi Bassarg E. M.,

Brandon R. R., Dayler S. P. A. Andrews Frankoch C., Baldain D.,

Brandon R. M., Basa A., Dastella R. A. Bang Maturgul Loi Bassarg E. M.,

Brandon R. M., Carlay S., Dalcher A., Davins B. D., Proceeding D., Brocketon P. Brothtar P. A.,

Rockety B. D., Becchan M. R., Bong J. B. Frocketon P., Brothtar P.,

Rockety B. D., Becchan M. R., Bong J. B., Brocketon P., Brothtar P.,

Rockety B. D., Becchan M. R., Bong J. B., Brocketon P., Brothtar P.,

Rockety B. D., Becchan M. R., Bong J. B., Brocketon P., Brothtar P.,

Rockety B. D., Becchan M. R., Bong J. W., Brocketon P., Brothtar P.,

Rockety B. D., Becchan M. R., Bong Z. M., Brocketon P., Brothtar P.,

Rockety B. D., Becchan M. R., Bong Z. M., Brocketon R., Davins P.,

Rockety B. D., Berchan M. R., Brocketon R., Brothtar B., Relact R.,

Rocket B. D., Berchan M. R., Brown M. R., Brocketon R., Brothtar B., Markel B.
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SEQUENCE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           RESULT 8
δλ
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        δ
                                                                        3;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Ξ,
                                                                                                                                                   1867 TITPATR------PQPSRQD-------VCDEEPAPGECSTWVLKWHFDRKI 1904
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1394 CHLPLDVGKCQGSFDSWYYEMATGSCVEFKYSGCSGNANRFASREECENTCV------ 1445
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1446 ------REPHSDTTSHGTSVCDEAKETGPCTNFATKWYYNKADGT 1486
                                                                                                                                                                                                                  69 TGDLATSRNAADSSVPSAPRRQDSEDHSSDMFNYEEYCTANAVTGPCRASFPRWYFDVER 128
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 "Cloning and characterization of thrombospondin, a novel multidomain glycoprotein associated with the gut of Haemonchus contortus."; Submitted (MAR-2001) to the EMBL/GenBank/DDBJ databases.

EMBL, AF04312; AAB99830.2; -.

HSSP; P05067; 1CA0.

InterPro; IPR000561; EGF-11ke.

InterPro; IPR000523; Kunitz_BPTI.

Ffam; PF00014; Kunitz_BPTI:

Pfam; PF00014; Kunitz_BPTI; 12.

Pfam; PF00090; tsp_1; 6.

PRINTS; PR00759; BASICPTASE.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               71 DLATSRNAADSSVPSAPRRQDSEDHSSDMFNYEEYCTANAVTGPCRASFPRWYFDVERNS 130
                                                                        Gaps
                                                                                                                   9 DFCLVSKVVGRCRASMPRWWYNVTDGSCQLFVYGGCDGNSNNYLTKEECLKKCATVTENA 68
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                11 CLVSKVVGRCRASMPRWWYNVTDGSCQLFVYGGCDGNSNNYLTKEECLKKCATVTENATG 70
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida; Strongylida;
Trichostrongyloidea; Haemonchidae; Haemonchinae; Haemonchus.
NCBI_TaxID=6289;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Length 1572;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Skuce P.J., Newlands G.F.J., Stewart M., Pettit D., Smith D.,
                         Length 3060;
                                                                      Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Serine protease inhibitor.
SEQUENCE 1572 AA; 171871 MW; 2260B30DC2F903EC CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Last sequence update)
Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match 27.1%; Score 256.5; DB 5; Best Local Similarity 30.1%; Pred. No. 2.1e-18; Matches 47; Conservative 21; Mismatches 61;
                                                                                                                                                                                                                                                                                                                                          129 NSCNNFIYGGCRGNKNSYRSEEACMLRCFRQQENPPLP 166
                    27.3%; Score 259; DB 5;
32.9%; Pred. No. 2.5e-18;
ive 16; Mismatches 66
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CNNFIYGGCRGNKNSYRSEEACMLRCFRQQENPPLP 166
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PRT; 1572 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Created)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PROSITE; PS50279; BPTI_KUNITZ_2; 6. PROSITE; PS50092; TSP1; 2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SMART; SM00001; EGF_like; 1.
SMART; SM00131; KU; 6.
SMART; SM00209; TSP1; 7.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              01-JUN-1998 (TrEMBLrel. 06, 01-JUN-2001 (TrEMBLrel. 17, 01-DEC-2001 (TrEMBLrel. 19, THROMBOSPONDIN.
                                               Best Local Similarity 32.9%
Matches 52; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Haemonchus contortus.
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SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  STRAIN-MOREDUN;
                         Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   044938
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                                                                                                                                                                                                                                                                                                                                                                                                                                    RESULT 6
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RESULT 7

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protein, accompanies morphogenesis of epithelial monolayers in Manduca
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     2186 -----SEAKITTTVR--PTEAHP----LTEMCFMEKDPGPCTDTETRWVYDYKL 2228
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TGDLATSRNAADSSVPSAPRRQDSEDHSSDMFNYEEYCTANAVTGPCRASFPRWYFDVER 128
                                                                                                                                    LACUNIN PRECURSOR.

Manduca sexta (Tobacco hawkmoth) (Tobacco hornworm).

Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;

Eukaryota; Neoptera; Endopterygota; Lepidoptera; Glossata; Ditrysia;

Sphingiodea; Sphingidae; Sphinginae; Manduca.

NCBI_TaxID=7130;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        9 DFCLVSKVVGRCRASMPRWWYNVTDGSCQLFVYGGCDGNSNNYLTKEECLKKCATVTENA 68
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            093424;
01-NOV-1998 (TrEMBLrel. 08, Created)
01-NOV-1998 (TrEMBLrel. 08, Last sequence update)
01-DEC-2001 (TrEMBLrel. 08, Last annotation update)
01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
HYPOTHETICAL 31-1 KDA PROTEIN.
Cyprinus carpio (Common carp).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Actinopterygii; Neopterygii; Teleostei; Euteleostei; Ostariophysi;
                                                                                                                                                                                                                                                                                                                               SEQUENCE FROM N.A.
MEDLINE-99457716; PubMed-10528409;
Nardi J.B., Martos R., Walden K.K., Lampe D.J., Robertson H.M.;
"Expression of lacunin, a large multidomain extracellular matrix
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Immunoglobulin domain; Serine protease inhibitor; Signal.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     63; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             11 POTENTIAL.
349364 MW; AB4ACD459C0D9134 CRC64;
                                                                                Last sequence update)
Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                2229 GKCVTFEYGGGGGNRNNFPTEEYCQYYCGTAQDICQLPMRS 2269
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                129 NSCNNFIYGGCRGNKNSYRSEEACMLRCFRQQENPPLPLGS 169
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        26.9%; Score 255; DB 5;
nilarity 31.7%; Pred. No. 6.9e-18;
Conservative 23; Mismatches 63
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Biol. 29:883-897(1999).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Pfam; PF00095; wap; 1.
PRINTS; PR00795; bASICPTASE.
SMART; SM00131; KU; 10.
SMART; SM00209; TSP1; 7.
SMART; SM00217; WAP; 1.
PROSITE; PS00317; 4_DISULFIDE_CORE; 1.
PROSITE; PS00279; BPTI_KUNITZ_1; 8.
PROSITE; PS50279; BPTI_KUNITZ_2; 10.
PROSITE; PS50092; TSP1; 1.
                                                         Created)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       EMBL; AF078161; AAF04457.1; --
HSSP; P12111; ZKWT.
InterPro; IPR004094; Ig_c2.
InterPro; IPR003599; Ig_c2.
InterPro; IPR003223; Kunitz_BPTI.
InterPro; IPR000884; TSPI.
InterPro; IPR000884; TSPI.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Pfam; PF02822; Antistasin; 4. Pfam; PF00047; ig; 2. Pfam; PF00014; Kunitz_BPTI; 9.
                                                01-MAY-2000 (TrEMBLrel. 13, 01-MAY-2000 (TrEMBLrel. 13, 01-DEC-2001 (TrEMBLrel. 19,
PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 3198 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Local Similarity
Les 51; Conserv
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2174 AA;
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SEQUENCE FROM N.A.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SEQUENCE
                                                                                                                                                               Query Match
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SMART;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Q9GQR0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Q9GQR0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SMART;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SMART;
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                                                                                                                                                                                                       Matches
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    DR
KW
FT
FT
SQ
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IS THAT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ---KEDKSP-----COLDDEPGPCRGLVPRYFFDFK 122
                                                                                                                                                                                                                                                                                                                                                                                                         Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       94
                                                                                                                                                                                                                                                                                                                                                                                                                                             8 HDFCLVSKVVGRCRASMPRWWYNVTDGSCQLFVYGGCDGNSNNYLTKEECLKKCATVTEN 67
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Caenorhabditis elegans.
Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida; Rhabditoidea;
Rhabditidae; Peloderinae; Caenorhabditis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    40;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  STRAIN-BRISTOL N2;
Geisel C., Bradshaw H.;
"The sequence of C. elegans cosmid C37C3.";
submitted (JUL-1996) to the EMBL/GenBank/DDBJ databases.
- - ALTERNATIVE PRODUCTS: TWO FORMS (A AND B) MAY BE PRODUCED:
ALTERNATIVE SPLICING OF THE SAME GENE. THE SEQUENCE SHOWN
                                                                                                                                                                                                                                                                                                                                                                   Length 287;
                                                                                                                                                                                                                                                                                                                                                                                                         Indels
                                                                                                Gracey A.Y.;
Submitted (JUN-1998) to the EMBL/GenBank/DDBJ databases.
EMBL, AF0086481; AAC19410.1; --
HSSP; P31713; 1SHP.
                                                                                                                                                                                                                                                        PROSTIE; PS00280; BPTL KUNITZ_1; 3. PROSITE; PS50279; BPTL_KUNITZ_2; 3. Hypothetical protein; Serine protease inhibitor. SEQUENCE 287 AA; 33093 MW; DF69B3D76718115E CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    123 SQECKRFFYGGCFGNANNFKTIKECHERCLPALNNMERNAPL 164
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             128 RNSCNNFIYGGCRGNKNSYRSEEACMLRCF----RQQENPPL 165
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Last sequence update)
Last annotation update)
                                                                                                                                                                                                                                                                                                                                                               Query Match 26.6%; Score 252; DB 13; 1
Best Local Similarity 30.9%; Pred. No. 8.8e-19;
Matches 50; Conservative 19; Mismatches 53;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        2167
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 HSSP; P00381; IDTK.
INTERPRO; IPR003598; Ig_C2.
INTERPRO; IPR003506; Ig_MHC.
INTERPRO; IPR003006; Ig_MHC.
INTERPRO; IPR000384; ISPI.
Flam; PF00047; Ig; I.
Pfam; PF00047; Ig; I.
Pfam; PF000047; Ig; II.
Pfam; PF000049; ISPI.; II.
Pfam; PF000090; ISPI.; II.
SMART; SM00131; KU; II.
SMART; SM00131; KU; II.
SMART; SM00209; ISPI.; II.
PROSITE; PS50279; BPTI.KUNITZ_1; IO.
PROSITE; PS50279; BPTI.KUNITZ_1; IO.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Created)
  Cyprinidae; Cyprinus
                                                                                                                                                                            InterPro; IPR002223; Kunitz_BPTI.
Pafan; PR00014; Kunitz_BPTI; 3.
PRINTS; PR00759; BASICPTASE.
SMART; SM00131; KU; 3.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             EMBL; U64857; AAC25868.1; -. EMBL; U64857; AAC25867.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        076840; Q22911;
01-NOV-1998 (TrEMBLrel. 08,
01-NOV-1998 (TrEMBLrel. 08,
01-DEC-2001 (TrEMBLrel. 19,
C37C3.6 PROTEIN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PRELIMINARY;
                                                        SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SEQUENCE FROM N.A.
Cypriniformes; C
NCBI_TaxID=7962;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           NCBI_TaxID=6239;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              OF FORM B.
                                                                             TISSUE=LIVER;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             C37C3.6
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Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;
Pterygota; Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
Ephydroidea; Drosophilidae; Drosophila
                                                                                                                                                                                                                                                                                     Gaps
                                                                                                                                                                                                                                                                                                                                          RSIHDFCLVSKVVGRCRASMPRWWYNVTDGSCQLFVYGGCDGNSNNYLTKEECLKKC--- 61
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ţ
PROSITE; PS50092; TSP1; 4.
Alternative splicing; Hypothetical protein; Immunoglobulin domain; Serine protease inhibitor.
VARSPLIC 147 155 MISSING (IN ISOFORM A).
VARSPLIC 155 AND SKR KDD - SKR (IN ISOFORM A).
VARSPLIC 1559 AND MISSING (IN ISOFORM A).
SEQUENCE 2167 AA; 237599 MW; 96274786D52E3639 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Kramerova I.A., Kawaguchi N., Nelson R.E., Fessler L.I., Chen Y., Kramer J.M., Ackley B.D., Sieron A.L., Prockop D.J., Fessler J.H.;

"Papilin in development; a pericellular protein with a homology to
                                                                                                                                                                                                                                                                                  6
                                                                                                                                                                                                                              Length 2167;
                                                                                                                                                                                                                           26.4%; Score 250.5; DB 5; Length 30.1%; Pred. No. 1.3e-17; ive 26; Mismatches 79; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            26 POTENTIAL.
231936 MW; 038F707952623120 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     116 RASFPRWYFDVERNSCNNFIYGGCRGNKNSYRSEEACMLRCFR 158
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    01-MAR-2001 (TrEMBLrel. 16, Last sequence update)
01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
EXTRACELLULAR MATRIX PROTEIN PAPILIN PRECURSOR.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Matrix protein; Serine protease inhibitor; Signal. SIGNAL 1 26
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Created)
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PROSITE; PS50092; TSP1; 3.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Flybase; FB90003137; Ppn. InterPro; IPR003599; Ig. InterPro; IPR003598; Ig. c2. InterPro; IPR003508; Ig_like. InterPro; IPR0020223; Kunitz_BPTI. InterPro; IPR000884; TSPI. InterPro; IPR002221; WAP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    STRAIN=DP CN BW;
MEDLINE=20530499; PubMed=11076767;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ADAMTS metalloproteinases.",
Development 127:5475-5485(2000).
EMBL, AR205357; AAG37995-1; ...
HSSP; P12111; 2KNT.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Pfam; PF00014; Kunitz_BPT1; 3.
PRINTS; PR00003; 4DISULPHCORE.
PRINTS; PR00759; BASICPTASE.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SM00408; IGC2; 2.
SM00410; IG_like; 1.
SM00131; KU; 3.
SM00209; TSP1; 7.
SM00217; WAP; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       01-MAR-2001 (TrEMBLrel. 16, 01-MAR-2001 (TrEMBLrel. 16, 01-DEC-2001 (TrEMBLrel. 19,
                                                                                                                                                                                                                                                     Local Similarity 30.1 es 49; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SMART; SM00409; IG; 3.
SMART; SM00408; IGc2;
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Caenorhabditis elegans
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Q28874
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Matches
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;
                                                                                                        69 TGDLATSRNAADSSVPSAPRRQDSEDHSSDMFNYEEYCTANAVTGPCRASFPRWYFDVER 128
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ---CNLPIVRGPCRAFIQLWAFDAVK 108
                                                Gaps
                                                                                 11 CLVSKVVGRCRASMPRWWYNVTDGSCQLFVYGGCDGNSNNYLTKEECLKKCATVTENATG 70
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  82
                                                                                                                                                               71 DLATSRNAADSSVPSAPRRQDSEDHSSDMFNYEEYCTANAVTGPCRASFPRWYFDVERNS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Homo sapiens (Human).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                28 DSCQLGYSAGPCMGMTSRYFYNGTSMACETFQYGGCMGNGNNFVTEKECLQTCRTVAA--
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    39;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        MEDLINE-91214554; PubMed-1708673; Vetr H., Gebhard W.; "Structure of the human alpha-1-microglobulin-bikunin gene."; EMBL; X54818; CAR4. HOSPe-Seyler 371:1185-1196(1990). HSSP: P02760; IBIK.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Length 151;
Length 2174;
                                         44; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   151 AA; 16542 MW; 88F400C5ECA19831 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                          01-NAY-1997 (TrEMBLrel. 03, Created)
01-NAY-1997 (TrEMBLrel. 03, Last sequence update)
01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
ALPHA-1-MICROGLOBULIN (FRAGMENT).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Last sequence update)
Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            DB 4;
  26.4%; Score 250; DB 5; 31.5%; Pred. No. 1.5e-17; ive 20; Mismatches 44
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        25.8%; Score 244.5; DB 4 32.4%; Pred. No. 2.6e-18;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               2225 AA.
                                                                                                                                                                                                                                                                                                                                                                                        151 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  14; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              109 GKCVLFPYGGCQGNGNKFYSEKECREYC 136
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     129 NSCNNFIYGGCRGNKNSYRSEEACMLRC 156
                                                                                                                                                                                                                                                                     Created)
                                                                                                                                                                                                                                              131 CNNFIYGGCRGNKNSYRSEEACMLRC 156
                                                                                                                                                                                                                                                                                                                                                                                          PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      InterPro; IPR002223; Kunitz_BPTI.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PROSITE; PS00280; BPTI_KUNITZ_1; PROSITE; PS50279; BPTI_KUNITZ_2; Serine protease inhibitor.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Pfam; PF00014; Kunitz_BPT1; PRINTS; PR000759; BASICPTASE. SMART; SM00131; KU; 2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                01-JUN-1998 (TrEMBLrel. 06, 01-JUN-1998 (TrEMBLrel. 06, 01-DEC-2001 (TrEMBLrel. 19, WOLF3.3.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Local Similarity 32.49
                                                                                                                                                                                                      1722 -----AASENLPT----
                                           46; Conservative
                                                                                                                                                                                                                                                                                                                                                                                        PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PRELIMINARY;
    Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        NCBI_TaxID=9606;
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045881;
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P78491
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045881
ID 04588
AC 04588
DT 01-JU
DT 01-JU
DT 01-DE
W01F3
GN W01F3
                                         Matches
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TGDLATSRNAADSSVPSAPRRQDSEDHSSDMFNYEEYCTANAVTGPCRASFPRWYFDVER 128
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Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida; Rhabditoidea;
Rhabditidae; Peloderinae; Caenorhabditis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 11 CLVSKVVGRCRASMPRWWYNVTDGSCQLFVYGGCDGNSNNYLTKEECLKKC--ATVTENA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Canis familiaris (Dog).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Carnivora; Fissipedia; Canidae; Canis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           32;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Length 2225;
                                                                                                                                                                                                                                                                                                                   Genome sequence of the nematode C.elegans: A platform for
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  25.3%; Score 240; DB 5; Length 22 ilarity 29.3%; Pred. No. 1.8e-16; Conservative 21; Mismatches 58; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Serine protease inhibitor.
SEQUENCE 2225 AA; 242198 MW; A5DDBAE9D2A7B02A CRC64;
                                                                                                                                                    Cummings P.N.;
Submitted (MAR-1997) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 01-NOV-1996 (TrEMBLrel. 01, Created)
01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
TISSUE FACTOR PATHWAY INHIBITOR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    129 NSCNNFIYGGCRGNKNSYRSEEACMLRCFRQQENPPL 165
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PROSITE; PS50280; BPTI KUNITZ_1; 8.
PROSITE; PS50279; BPTI_KUNITZ_2; 10.
PROSITE; PS00484; THYROGLOBULIN_1; UNKNOWN_1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                396 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                   InterPro; IPR002899; EB.
InterPro; IPR002223; Kunitz_BPTI.
InterPro; IPR000716; Thyroglobulin_1.
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EMBL; S75369; AAB22443.1; --
HSSP; P10646; LIFX.
INTEXPRO; IPR002223; Kunitz_BPTI.
Pfam; PF00014; Kunitz_BPTI; 3.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Pfam; PF00014; Kunitz_BPII; 10. Pfam; PF00086; thyroglobulin_1;
                                                                                                                                                                                                                                                                                                                                          investigating biology.";
Science 282:2012-2018(1998).
EMBL; 292815; CAB07294.1; -.
HSSP; P31713; 1SHP.
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SMART; SM00211; TY; 1.
SMART; SM00289; WR1; 4.
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                                                                                              [1]
SEQUENCE FROM N.A.
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SEQUENCE FROM N.A.
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                                                              NCBI_TaxID=6239;
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Best Loca
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Q925W1
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     SO KW
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KAWAI J., Shinagawa A., Shibata K., Yoshino M., Itoh M., Ishii Y., Rawai J., Shinagawa A., Shibata K., Yoshino M., Itoh M., Ishii Y., Rawai J., Shinagawa A., Fukudishi Y., Randola K., Yondo S., Yamanaka I., Alzawa M., Mishi K., Kyosawa H., Rondo S., Yamanaka I., Radota K., Matsuka H., Ashburner M., Batalov S., Casavant T., Radota K., Matsud H.A., Ashburner M., Batalov S., Casavant T., Relischmann W., Gasterland T., Gissi C., King B., Rochiwa H., Schriml L., K., Stulis R., Tomita M., Wagner L., Washio T., Sakai K., Okido T., Furuno M., Aono H., Baldarelli R., Barsh G., Sakai K., Okido T., Furuno M., Aono H., Baldarelli R., Barsh G., Barke J., Boffelli D., Bojunga N., Carninci P., de Bonaldo M.F., Bromstein M.J., Bult C., Fletcher C., Fujita M., Gariboldi M., Gustincich S., Hill D., Hofmann M., Hume D.A., Kamiya M., Lee N.H., A Lyons P., Marchionni L., Mashima J., Mazzarelli J., Mombaerts P., Nordone P., Ring B., Ringwald M., Rodriguez I., Sakamoto N., Sasaki H., Sato K., Schoenbach C., Seya T., Shibata Y., Storch K.-F., Whyshaw Boris A., Yoshida K., Hasegawa Y., Kawaji H., Kohtsuki S., Hayashizani Y.; Kawaji H., Kohtsuki S., Hayashizani Y., Kawaji H., Kohtsuki S., Mayashizani Y., Kawaji H., Kohtsuki S.,
                                                                                                                                                                                                                                                                                                                                               65 TENATGDLATSRNAADSSVPSAPRRQDSEDHSSDMFNYEEYCTANAVTGPCRASFPRWYF 124
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ---KTETLEKVLEKPDYCHMNEDSGLCRGFVTRYYY 143
                                                                                                                                                                                                                                                                                                            5 RSIHDFCLVSKVVGRCRASMPRWWYNVTDGSCQLFVYGGCDGNSNNYLTKEECLKKCATV 64
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   "Functional annotation of a full-length mouse cDNA collection."; Nature 409:685-690(2001).
BMBL; AKO04907; BAB23659.1; -.
HSSP; PO2766; 1BIK.
                                                                                                                                                                                                Length 396;
                       SMART; SM00131; KU; 3.
PROSITE; PS00280; BPTL KUNITZ_1; 3.
PROSITE; PS50299; BPTL KUNITZ_2; 3.
SELIME professe inhibitor.
SEQUENCE 396 AA; 43948 MW; 50F65C8337A003D9 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       01-JUN-2001 (TrEMBLrel. 17, Created)
01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
                                                                                                                                                                                             Match 25.3%; Score 239.5; DB 6; Local Similarity 29.6%; Pred. No. 2.7e-17; les 45; Conservative 24; Mismatches 60;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        349 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    125 DVERNSCNNFIYGGCRGNKNSYRSEEACMLRC 156
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  MGD; MGI:88002; Ambp.
InterPro; IPR002223; Kunitz_BPTI.
InterPro; IPR002345; Lipocalin.
InterPro; IPR000546; Lipocalin.
InterPro; IPR000566; Lipocalin.
Pfam; PF00061; Ilpocalin; 1.
PRINTS; PR00759; BASICPPASE.
PRINTS; PR00179; LIPOCALIN.
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PROSITE; PS50279; BPTI_KUNITZ_2;
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PRINTS; PR00759; BASICPTASE.
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MEDLINE=99326507; PubMed=10395906; Lindqvist A., Rouet P., Salier J.P., Akerstrom B.; The alphal-microglobulin/bikunin gene: characterization in mouse and evolution ":
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                                                                                                                                                                                                                                                                                69 TGDLATSRNAADSSVPSAPRRQDSEDHSSDMFNYEEYCTANAVTGPCRASFPRWYFDVER 128
                                                                                                                                                                                                                                                                                                                         -- CNLPIVOGPCRAFIKLWAFDAAQ 308
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              228 DSCOLNYSEGPCLGMOERYYYNGASMACETFOYGGCLGNGNNFISEKDCLOTCRTIAA-- 285
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               69 TGDLATSRNAADSSVPSAPRRQDSEDHSSDMFNYEEYCTANAVTGPCRASFPRWYFDVER 128
                                                                                                                                                                                      9 DFCLVSKVVGRCRASMPRWWYNVTDGSCQLFVYGGCDGNSNNYLTKEECLKKCATVTENA 68
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Gaps
                                                                                                                                                                                                                 Mus musculus (Mouse).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Musinae; Mus.
NCBI_TaxID=10090;
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                                                                                            DB 11; Length 349;
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                                                                                         24.8%; Score 235.5; DB 11; Length 29.7%; Pred. No. 6.2e-17; ive 18; Mismatches 47; Indels
                                              E593222FBC01BC3D CRC64;
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01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
ALPHA-1-MICROGLOBULIN/BIKUNIN PRECURSOR.
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Job time : 33 secs
PROSITE; PS00213; LIPOCALIN; UNKNOWN_1.
Serine protease inhibitor.
SEQUENCE 349 AA; 39101 MW; E5932225
                                                                                                                                                                                                                                                                                                                                                                          129 NSCNNFIYGGCRGNKNSYRSEEACMLRC 156
                                                                                                                                                                                                                                                                                                                                                                                                     309 GKCIOFHYGGCKGNGNKFYSEKECKEYC 336
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39029 MW;
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29.7%;
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SATOR 234:329-336(1999).
EMBL; AF034692; AAD01995.1;
STGNAL.
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Best Local Similarity 29.7%
                                                                                                                                          44; Conservative
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                                                                                                                                                                                                                                                                                                                              286 -----
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                                                                                              Query Match
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GenCore version 5.1.3
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OM protein - protein search, using sw model

October 18, 2002, 10:33:48; Search time 12 Seconds (without alignments) 548.527 Million cell updates/sec Run on:

Title: Perfect score: Sequence:

US-09-218-913D-52 948 1 ADRERSIHDFCLVSKVVGRC......ACMLRCFRQQENPPLPLGSK 170

BLOSUM62 Gapop 10.0 , Gapext 0.5 Scoring table:

105224 seqs, 38719550 residues Searched:

105224 Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0 Maximum DB seq length: 20000000000

Post-processing: Minimum Match 08
Maximum Match 1008
Listing first 45 summaries

SwissProt\_40:\* Database : Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

Description	043291 homo sapien	mus m	043278 homo sapien	7 mus m	O54819 mus musculu	3 pos	meri		P13371 Ovis aries	P02760 homo sapien	oryct		P04365 equus cabal		Q28864 macaca mula		Q07456 mus musculu	P10646 homo sapien	homod			Q06481 homo sapien	Q03610 caenorhabdi			P05067 homo sapien		P36992 pleuronecte	P81162 boophilus m		P53601 macaca fasc	P82968 melithaea c	P81547 anthoplieura
ID	SPT2_HUMAN	SPT2_MOUSE	SPT1_HUMAN	SPT1_MOUSE	TFPI_MOUSE	AMBP_BOVIN	AMBP_MERUN	TFPI_RAT	IATR_SHEEP	AMBP_HUMAN	TFPI_RABIT	AMBP_PIG	IATR_HORSE	AMBP_RAT	TFPI_MACMU	AMBP_MESAU	AMBP_MOUSE	TFPI_HUMAN	TFP2_HUMAN	APP2_RAT	TFP2_MOUSE	APP2_HUMAN	YN81_CAEEL	A4_RAT	A4_SAISC	A4_HUMAN	A4_MOUSE	AMBP_PLEPL	CRPT_BOOMI	A4_MACMU	A4_MACFA	MCPI_MELCP	AXP1_ANTAF
th DB	 252 1																	304 1													87 1		
% Query Match Length	 100.0																																
Score	 948	663	312	294	259.5	249.5	247.5	246.5	244.5	244.5	244	242.5	241.5	237.5	236.5	235.5	235.5	233.5	214.5	210	204.5	200	191	187.5	186		183.5	181.5	175.5	174.5	174.5	171.5	170
Result No.	 Н,	7	m	4	S	9	7	89	o	10	11	12	13	14	15	16	17	18	19	20	21	22	23	24	25	56	27	28	29	30	31	32	33

P10280 anemonia su	Q29428 ovis aries P49223 homo sapien	Q28201 bos taurus Q9bd}1 macaca mula	P00975 bos taurus P04815 bos taurus	P16044 tachypleus P00974 bos taurus	P00992 vipera ammo Q9da01 mus musculu
IP52_ANESU	TKD1_SHEEP	TKD1_BOVIN	IBPS_BOVIN BPT2_BOVIN	IBPI_TACTR BPT1_BOVIN	IVB3_VIPAA EPPI_MOUSE
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62	265	164	100	61 100	65 134
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17.	16.	16.	16.4	16. 16.	16. 16.
167	159	155.5	155	153 152.5	152 152
3.5	36	398	40	42	44 45

## ALIGNMENTS

RESULT 1  SPT2_HUMAN  AC OCT  DT 16-0C  EURARY  OCC EURARY  RR MEDLII  RE MEDLII
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190

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1 ADRERSIHDFCLVSKVVGRCRASMPRWWYNVTDGSCQLFVYGGCDGNSNNYLTKEECLKK 60
activator inhibitor type 2) (HAI-2)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Matches 116; Conservative
          SPINT2 OR HAIZ.
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          for commercial
                  (See http://www.isb-sib.ch/announce/
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    61 CATVTENATGDLATSRNAADSSVPSAPRRQDSEDHSSDMFNYEEYCTANAVTGPCRASFP 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               87
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SPT2_MOUSE STANDARD; PRT; 252 AA.
09W103; Q9W104; Q9W105;
16-OCT-2001 (Rel. 40, created)
16-OCT-2001 (Rel. 40, Last sequence update)
16-OCT-2001 (Rel. 40, Last annotation update)
Kunitz-type protease inhibitor 2 precursor (Hepatocyte growth factor
as its content is in
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1 ADRERSIHDFCLVSKVVGRCRASMPRWWYNVTDGSCQLFVYGGCDGNSNNYLTKEECLKK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        28 ADRERSIHDFCLVSKVVGRCRASMPRWYNVTDGSCQLEVYGGCDGNSNNYLTKEECLKK
                                                                                                                                                                                                                                                                                                                                                                  . . .).
                                                                                                                                                                             PROSITE; PS00280; BPTI_KUNITZ_1; 2.
PROSITE; PS50279; BPTI_KUNITZ_2; 2.
Serine protease inhibitor; Repeat; Glycoprotein; Transmembrane;
Signal; Polymorphian
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REACTIVE BOND (BY SIMILARITY).
N'LINKED (GLCNAC. . .).
V'LINKED (GLCNAC. . .) (POTENTIA
                                                                                                                                                                                                                           KUNITZ-TYPE PROTEASE INHIBITOR
EXTRACELLULAR (POTENTIAL).
POTENTIAL.
          Usage by and
                                                                                                                                                                                                                                                                                                                                                                                                                                                            Length 252;
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REACTIVE BOND (BY SIMILARITY).
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R -> P (IN REF. 1).
R -> K (IN REF. 3).
D -> H (IN REF. 3).
A7D3360C0EECAB2B CRC64;
                                                                                                                                                                                                                                                        CYTOPLASMIC (POTENTIAL).
BPTI/KUNITZ INHIBITOR 1.
BPTI/KUNITZ INHIBITOR 2.
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0
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Pred. No. 3.1e-83;
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Q -> H (IN REF. 3)
R -> P (IN REF. 1)
R -> K (IN REF. 3)
D -> H (IN REF. 3)
use by non-profit institutions as long a modified and this statement is not removed. entities requires a license agreement (See )
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                 entities requires a license agreement ( or send an email to license@isb-sib.ch)
                                                                                                                                          InterPro; IPR002223; Kunitz_BPTI.
                                                              AF027205; AAB84031.1;
BC001668; AAH01668.1;
BC007705; AAH07705.1;
BC011951; AAH11951.1;
BC011955; AAH11955.1;
BC012868; AAH12868.1;
                                             EMBL; AB006534; BAA25024.1; -. EMBL; U78095; AAC02781.1; -.
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100.0%;
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                                                                                                                                                  Pfam; PF00014; Kunitz_BPTI;
PRINTS; PR00759; BASICPTASE.
SMART; SM00131; KU; 2.
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Best Local Similarity 100.
Matches 170; Conservative
                                                                                                                       P05067; 1TAW.
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252 AA;
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CONFLICT
CONFLICT
SEQUENCE
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ACT_SITE
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CARBOHYD
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EMBL;
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                                                                                   EMBL;
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SPT2_MOUSE
                                                                                             EMBL;
                                                                                                                         HSSP;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      88
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                                                                                                                                                                                               Itoh H., Kataoka H., Hamasuna R., Kitamura N., Koono M.;
"Hepatocyte growth factor activator inhibitor type 2 lacking the first
Kunitz-type serine proteinase inhibitor domain is a predominant
                                                                                                                                                                                                                                                                                                                                                                                                                               -!- TISSUE SPECIFICITY: ISOFORM 2 IS MORE PREDOMINANTLY EXPRESSED THAN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Gaps
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N-LINKED (GLCNAC. .) (POTENTIAL).

N-LINKED (GLCNAC. .) (POTENTIAL).

N-SINKE (IN ISOPORM 2 AND ISOFORM 3).

PRKQSAEDLSAEIFN -> CFVELSVAALFLEYA (IN
                                                                                                                                                                                                                                                                                                                                                   -!- SUBCELLULAR LOCATION: Type I membrane protein (Potential).
-!- ALTERNATIVE PRODUCTS: 3 ISOFORMS; 1 (SHOWN HERE), 2 AND 3; ARE PRODUCED BY ALTERNATIVE SPLICING.
                     Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PROSITE; PS00280; BPTL_KUNITZ_1; 2.
PROSITE; PS00280; BPTL_KUNITZ_2; 2.
Scrine protease inhibitor; Repeat; Glycoprotein; Transmembrane; Signal; Alternative splicing. Poprental.
                                                                                                                                                                                                                                                                                                                                                                                                                                                 ISOFORM 1.
-!- DOMAIN: THIS INHIBITOR CONTAINS TWO INHIBITORY DOMAINS.
-!- SIMILARITY: CONTAINS 2 BPTI/KUNITZ INHIBITOR DOMAINS.
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REACTIVE BOND (BY SIMILARITY).
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B2FF4B86924D4F8F CRC64;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CYTOPLASMIC (POTENTIAL).
BPTI/KUNITZ INHIBITOR 1.
BPTI/KUNITZ INHIBITOR 2.
                                                                                                                                                                                                                                                                            product in mouse but not in human.";
Biochem. Biophys. Res. Commun. 255:740-748(1999).
-!- FUNCTION: INHIBITOR OF HGF ACTIVATOR.
                                                                                                                        SEQUENCE FROM N.A., AND ALTERNATIVE SPLICING
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          BY SIMILARITY.
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                                                                                                                                                                          MEDLINE=99160423; PubMed=10049781;
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InterPro: IPR002223; Kunitz_BPTI.
Jefm; FR00014; Kunitz_BPTI; 2.
PRINTS; PR00759; BASICPTASE.
SMART; SM00131; KU; 2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             EMBL; AF099016; AAD22172.1; -. EMBL; AF099019; AAD22173.1; -. EMBL; AF099020; AAD22174.1; -. HSSP; P05067; 1TAM.
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Mus musculus (Mouse).
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                                                                         NCBI_TaxID=10090;
                                                                                                                                                   STRAIN=BALB/C;
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TRANSMEM
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PROSITE;
PROSITE;
PROSITE;
PROSITE;
                                                                                                     SIGNAL
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Matches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      MEDLINE-99303582; PubMed-10373425;
Lin C.Y., Anders J., Johnson M., Dickson R.B.;
"Purification and characterization of a complex containing matriptase
and a Kunitz-type serine processe inhibitor from human milk.";
J. Blol. Chem. 274:18237-18342(1999).
                                                                                Shimomura T., Denda K., Kitamura A., Kawaguchi T., Kito M., Kondo J., Kagaya S., Qin L., Takata H., Miyazawa K., Kitamura N.; "Hepatocyte growth factor activator inhibitor, a novel Kunitz-type serine protease inhibitor.";
                     87
                                                                                                                                                                                                                                                                                                                    16-OCT-2001 (Rel. 40, Created)
16-OCT-2001 (Rel. 40, Last sequence update)
01-MR-2002 (Rel. 41, Last annotation update)
Kunitz-type protease inhibitor 1 precursor (Hepatocyte growth factor
activator inhibitor type 1) (HAI-1).
CATVTENATGDLATSRNAADSSVPSAPRRQDSEDHSSDMFNYEEYCTANAVTGPCRASFP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          RWYFDVERNSCNNFIYGGCRGNKNSYRSEEACMLRCFRQQENPPLPLGSK 170
                                                                                                                                                                Strausberg R.; Submitted (MAR-2001) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                  513 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PARTIAL SEQUENCE, AND CHARACTERIZATION
                                                                                                                                                                                                                                                                                    PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         J. Biol. Chem. 272:6370-6376(1997).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SEQUENCE FROM N.A. MEDLINE=97197808; PubMed=9045658;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               InterPro; IPR002223; Kunitz_BPTI.
InterPro; IPR002172; LDL_recept_A.
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Pfam; PF00057; Idl_recept_a; 1.
PRINTS; PR00759; BASICPTASE.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   EMBL; AB000095; BAA25014.1; -. EMBL; BC004140; AAH04140.1; -.
                                                                                                                                                                                                                                                                                    STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SM00192; LDLa; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                              Homo sapiens (Human).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SM00131; KU;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           P31713; 1SHP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             NCBI_TaxID=9606;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TISSUE=Colon
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              605123
                                                                                                                                                                                                                                                                                SPT1_HUMAN
043278;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TISSUE-Milk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SMART;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SMART;
                                                                                                                                                                                                                                                             L_HUMAN
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               364 QRIHPPSDKGHCVDLPDTGLCKESIPRWYNPFSEHCARFTYGGCYGNKNNFEEEGQQCLE 423
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Itoh H., Kataoka H., Koono H.;
Mouse hepatocyte growth factor activator inhibitor type 1 (HAI-1).";
Submitted (MAR-1999) to the EMBL/GenBank/DDBJ databases.
-!- FUNCTION: INHIBITOR OF HGF ACTIVATOR (BY SIMILARITY).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        244 KQTEDYCLASNKVGRCRGSFPRWYYDPTEQICKSFVYGGCLGNKNNYLREBECILACRGV 303
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        16-OCT-2001 (Rel. 40, Last sequence update)
16-OCT-2001 (Rel. 40, Last annotation update)
Kunitz-type protease inhibitor 1 precursor (Hepatocyte growth factor activator inhibitor type 1) (HAI-1).
SPINTI OR HAII.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    5 RSIHDFCLVSKVVGRCRASMPRWWYNVTDGSCQLFVYGGCDGNSNNYLTKEECLKKCATV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 304 QGPSMERRHPVCSGTCQPTQFRCSNGCCIDSFLECDDTPNCPDASDEAACEKYTSGFDEL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           EE-----YCTANAVTGPCRASFPRWYFDVERNSCNNFIYGGCRGNKNSYRSEEACML
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Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      -TENATGDLATSRNAADS----SVPSAPRRQDS---EDHSSDMFNY
                                                                                                                                                                                                                                                                                                                                                            REACTIVE BOND (BY SIMILARITY).
N-LINKED (GLCNAC. .) (POTENTIAL).
N-LINKED (GLCNAC. .) (POTENTIAL)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          38;
                                                                                                                                                                                                                                                                                                                                                                                                                                 (POTENTIAL)
                                                                                                                              ä
                                                                                                                            KUNITZ-TYPE PROTEASE INHIBITOR BPTI/KUNITZ INHIBITOR 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              --- FUNCTION: INHIBITOR OF HGE ACLIVATOR.
--- SUBCELLULAR LOCATION: Secreted (By similarity).
--- DOMAIN: THIS INHIBITOR CONTAINS TWO INHIBITORY DOMAINS.
--- SIMILARITY: CONTAINS 1 LDL-RECEPTOR CLASS A DOMAIN.
--- SIMILARITY: CONTAINS 2 BPTI/KUNITZ INHIBITOR DOMAINS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Length 513;
                                                                                                                                                                                                                                                                                 SIMILARITY)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          71; Indels
                                                                                    Repeat; Glycoprotein; Signal
                                                                                                                                                                                 BPTI/KUNITZ INHIBITOR 2.
BY SIMILARITY.
BY SIMILARITY.
BY SIMILARITY.
REACTIVE BOND (BY SIMILARI BY SIMILARIY.
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BY SIMILARITY.
BY SIMILARITY.
                                                                                                                                                                                                                                                                                                                                                                                                                               N-LINKED (GLCNAC. . .) (P
D6E05F3A5885CDDD CRC64;
                                                                                                                                                                        LDL-RECEPTOR CLASS A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           7 Match 32.9%; Score 312; DB 1;
Local Similarity 33.5%; Pred. No. 2.3e-22;
nes 67; Conservative 24; Mismatches 71.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             507 AA.
BPTI_KUNITZ_1;
BPTI_KUNITZ_2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                     56885 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           RC-----FRQQENPPLP 166
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SCRGISKKDVFGLRREIPIP 443
                                          LDLRA_1;
LDLRA_2;
                                                                                    inhibitor;
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                      PS50279;
PS01209;
PS50068;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SEQUENCE FROM N.A. STRAIN=BALB/C;
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513
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                                                                                                                                                250
318
375
                                                                                      Serine protease
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Q9R097;
                                                                                                                                                                                                                                  DISULFID
DISULFID
ACT_SITE
DISULFID
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ACT_SITE
CARBOHYD
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SEQUENCE
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         modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
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054819; Q92208;
16-OCT-2001 (Rel. 40, Last sequence update)
16-OCT-2002 (Rel. 41, Last annotation update)
01-MAR-2002 (Rel. 41, Last annotation update)
associated coagulation inhibitor precursor (TFPI) (Lipoprotein-associated coagulation inhibitor) (LACI) (Extrinsic pathway inhibitor)
(EPI).
                                                                                                                                                                                                                                                                                                                                                                                                                                                          ::|| :::|
302 PKRHHPVCSGSCHATQFRCSNGCSIDGFLECDDTPDCPDGSDEATCEKYTSGFDELQNIH 361
                                                                                                                                                                                                                                                                                                                                                                                                                   Gaps
                                                                                                                                                                                                                                                                                                                                                                                                        DFCLVSKVVGRCRASMPRWWYNVTDGSCQLFVYGGCDGNSNNYLTKEECLKKCATV---- 64
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               362 FLSDKGYCAELPDTGFCKENIPRWYNPFSERCARFTYGGCYGNKNNFEEEQQCLESC 419
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    105 -----YCTANAVTGPCRASFPRWYFDVERNSCNNF1YGGCRGNKNSYRSEEACMLRC 156
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Craniata; Vertebrata; Euteleostomi;
Sciurognathi; Muridae; Murinae; Mus
                                                                                                                                                                                                                                                                                                                REACTIVE BOND (BY SIMILARITY).
N-LINKED (GLCNAC. ..) (POTENTIAL)
N-LINKED (GLCNAC. ..) (POTENTIAL)
20CB5DEDCEF46AA7 CRC64;
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  as its content is
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                                                                                                                                                                                                                BPTI/KUNTZ INHIBITOR 1.
LDL-RECEPTOR CLASS A.
BPTI/KUNTZ INHIBITOR 2.
BY SIMILARITY.
                                                                                                                                                                                                        KUNITZ-TYPE PROTEASE INHIBITOR
                                                                                                                                                                                                                                                                                                                                                                   Length 507;
                                                                                                                                                                                                                                                                                                                                                                                     66; Indels
                                                                                                                                             PROSITE; PS00280; BPTI_KUNITZ_1; 2.
PROSITE; PS50279; BPTI_KUNITZ_2; 2.
PROSITE; PS50068; LDLRA_1; FALSE_NEG.
PROSITE; PS50068; LDLRA_2; 1.
Serine protease inhibitor; Repeat; Glycoprotein; Signal.
SIGNAL
                                                                                                                                                                                                                                                                                                                                                                  31.0%; Score 294; DB 1;
33.1%; Pred. No. 1.2e-20;
ive 23; Mismatches 66
non-profit institutions as long
                                                        HSSP, P05067; ITAW.
MCD: MGI:1338033; Spint1.
Interpro; IPR002213; Kunitz_BPTI.
Interpro; IPR002172; LDL_recept_A.
Pfam; PF00014; Kunitz_BPTI; 2.
Pfam; PF00057; ldl_recept_a: 1.
PRINTS; PR00759; BASICPTASE.
SWART; SW00131; KU; 2.
SWART; SW00192; LDLa: 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE FROM N.A. (ISOFORM ALPHA).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      STRAIN=129;
MEDLINE=98152575; PubMed=9493581;
                                              EMBL; AF099018; AAF02490.1; -. HSSP; P05067; 1TAW.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Eukaryota; Metazoa; Chordata;
Mammalia; Eutheria; Rodentia;
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294
348
419
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4115
2380
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                                                                                                                                                                                                                                                                                                                            229
501
507 AA;
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les 59; Conser
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          NCBI_TaxID=10090;
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ACT_SITE
DISULFID
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DISULFID
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CARBOHYD
SEQUENCE
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Matches
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BPTI/KUNITZ INHIBITOR 2
(FACTOR X(A) BINDING SITE).
BPTI/KUNITZ INHIBITOR 3.
BY SIMILARITY.
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PROSITE; PS50279; BPTI_KUNITZ_2; 3.
Serine protease inhibitor; Glycoprotein; Repeat; Blood coagulation; Signal; Alternative splicing.

BY SIMILARITY.
    Oliver J.A., Liles D.K., Roberts H.R.; characterization of mouse tissue factor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          MISSING (IN ISOFORM BETA).
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D3EA3297E4B6A359 CRC64;
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                                                                                      pathway inhibitor (TFPI).";
Thromb. Haemost. 79:306-309(1998).
                                                                                                                                                                                                                SEQUENCE FROM N.A. (ISOFORM BETA).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    MGD; MGI:1095418; Tfpl.
InterPro; IPR002223; Kunitz_BPTI.
Pfam; PF00014; Kunitz_BPTI; 3.
PRINTS; PR00759; BASICPTASE.
SMART; SM00131; KU; 3.
                                                                                                                                                                                                                                                   MEDLINE=99138770; PubMed=9974373;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               EMBL; AF004833; AAC40035.1; -. EMBL; AF016313; AAD01586.1; -. HSSP; P10646; 1TFX.
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68
34987 M
Chang J.-Y., Monroe D.M., Cloning, expression, and pathway inhibitor (TFPI)."
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68
306 AA;
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CONFLICT
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CARBOHYD
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CARBOHYD
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BINDING
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CHAIN
CHAIN
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3,
                                                                                                                                                                                                                                                                                                                                                                                      AMBP_BOVIN STANDARD; PRT; 352 AA.
P00978; P35420; Q208020;
21-JUL-1986 (Rel. 01, Created)
01-NOV-1997 (Rel. 35, Last sequence update)
16-CCT-2001 (Rel. 40, Last annotation update)
AMBP protein precursor [Contains: Alpha-1-microglobulin; Inter-alpha-trypsin inhibitor light chain (ITI-LC) (Bikunin) (HI-30) (BI-14)
(Cumulus extracellular matrix stabilizing factor) (ESF)].
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Lindqvist A., Aakerstroem B.; "Bovine alpha 1-microglobulin/bikunin. Isolation and characterization of liver cDNA and urinary alpha 1-microglobulin."; Biochim. Biophys. Acta 1306:98-106(1996).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Chen L., Mao S.J.T., Larsen W.J.; "Identification of a factor in fetal bovine serum that stabilizes the cumulus extracellular matrix. A role for a member of the inter-alpha-
                                                       Gaps.
                                                                                                                    179 SPVNEVQMSDYVTDGNTVTDRSTVNNIVVPQSPKVPRRRD-----YRGRPWCLQPAD 230
                                                                                              63
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 oţ
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        proteolysis of the from bovine
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Bos taurus (Bovine).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovoidea;
                                                                                           DFCLVSKVVGRCRASMPRWWYNVTDGSCQLFVYGGCDGNSNNYLTKEECLKKCAT----
                                                                                                                                                                         ------VTE-NATGDLATSRNAADSSVPSAPRRQDSEDHSSDMFNYEEYCTANAV
                                                       25;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ŘEÁCTIVE SITES.
MEDLINE-84133808; Pubmed-6199276;
Hochstrasser K., Albrecht G.J., Schoenberger O.L., Wachter
                  Length
                                                       Indels
                                                                                                                                                                                                                                                                           112 TGPCRASFPRWYFDVERNSCNNFIYGGCRGNKNSYRSEEACMLRC 156
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Hochstrasser K., Wachter E., "Kunitz-type proteinase inhibitors derived by limited the inter-alpha-trypsin inhibitor, VII. Determination amino-acid sequence of the trypsin-released inhibitor inter-alpha-trypsin inhibitor.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Hoppe-Seyler's Z. Physiol. Chem. 364:1679-1687(1983)
                ; DB 1;
                                                       Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Biol. Chem. Hoppe-Seyler 366:473-478(1985).
                259.5;
No. 1.3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Biol. Chem. 267:12380-12386(1992)
                Score Pred. 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  MEDLINE=85225967; PubMed=2408637;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             MEDLINE=84133807; PubMed=6199275;
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MEDLINE=92291130; PubMed=1376324;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             MEDLINE=96201710; PubMed=8611630;
                                                       21;
                27.4%;
33.3%;
                                                     55; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             inhibitor family
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Bovidae; Bovinae; Bos.
NCBI_TaxID=9913;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE OF 206-219.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SEQUENCE OF 227-349
                Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   AMBP OR ITIL.
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                                                       Matches
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the inter-alpha-trypsin inhibitor, VII. Characterization of the bovine inhibitor as double headed trypsin-elastase inhibitor."; Hoppe-Seyler 8. Z. Physiol. Chem. 364:1689-1696(1983).
-!- FUNCTION: ALPHA-1-MICROGLOBULIN OCCURS IN MANY PHYSIOLOGICAL FLUIDS INCLUDING PLASMA, URINE, AND CEREBROSPINAL FLUID. IT APPEARS NOT ONLY AS A FREE MONOMER BUT ALSO IN COMPLEXES WITH IGA
οĘ
                                                                                                                                                                                                                                                                                                                                                         FUNCTION: INTER-ALPHA-TRYPSIN INHIBITOR, PRESENT IN PLASMA AND URINE, INHIBITS TRYPSIN, PLASMIN, AND LYSOSOMAL GRANULOCYTIC
    proteinase inhibitors derived by limited proteolysis
                                                                                                                                                                                                                                                                                                           AND ALBUMIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                 ELASTASE.
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C. --- FUNCTION: MAY DIFFUSE INTO FOLLICULAR FLUID AFTER AN OVULATORY STIMULUS TO ACT AS STRUCTURAL LINKER THAT ENSURE NORMAL CUMULUS EXPANSION, THROUGH STABILIZATION OF THE CUMULUS EXTRACELLULAR MATRIX THUS SUPPORTING THE PROCESS OF OVULATION.

--- SUBUNIT: I -ALPHA I plasma protease inhibitors are assembled from one or two heavy chains (Hi, H2 or H3) and one light chain, bikunin. Inter-alpha-inhibitor (I-ALPHA-I) is composed of H1, H2 and bikunin, and pre-alpha-inhibitor (I-ALPHA-I) of H3 and bikunin (By similarity).

--- PTM: THE PRECURSOR IS PROTEOLYTICALLY PROCESSED INTO TWO SEPARATELY FUNCTIONING PROTEINS.

--- PTM: Alpha-I-microglobulin contains a covalently linked brown-byllory and bikunin. Interprecessing the process of th

SIMILARITY: IN THE N-TERMINAL SECTION; BELONGS TO THE LIPOCALIN

-!- SIMILARITY: CONTAINS 2 BPTI/KUNITZ INHIBITOR DOMAINS

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Signal; Serine protease inhibitor; HSSP, P02760; 1BIK.
InterPro; IPR002223; Kunitz\_BPTI.
InterPro; IPR002345; Lipocalin.
InterPro; IPR00545; Lipocalin.
InterPro; IPR00546; Lipocalin.
Pfam; PF00014; Kunitz\_BPTI; 2.
Pfam; PF00061; lipocalin; 1.
PRINTS; PR00759; BASICPTASE.
PRINTS; PR00179; LIPOCALIN.
SMART; SM00119; LIPOCALIN. PROSITE; PS00280; BPTL KUNITZ\_1; 2. PROSITE; PS50279; BPTL\_KUNITZ\_2; 2. PROSITE; PS00213; LIPOCALIN; 1. EMBL; U35642; AAB07599.1; -. 19 203 352 Glycoprotein; Plasma; Lipocalin. A01209; TIBOBI. 1 20 206

BY SIMILARITY.
RY SIMILARITY.
ELASTASE).

INHIBITORY SITE (P1) (TRYPSIN).
N-LINKED (GLCNAC. .) (POTENTIAL).
N-LINKED (GLCNAC. .) (POTENTIAL).
N-LINKED (GLCNAC. .).

LIGHT

ALPHA-1 MICROGLOBULIN. INTER-ALPHA-TRYPSIN INHIBITOR

BPTI/KUNITZ INHIBITOR 2. CHROMOPHORE (BY SIMILARITY).

BPTI/KUNITZ INHIBITOR 1. BPTI/KUNITZ INHIBITOR 2.

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SUBUNIT: I-ALPHA-I plasma protease inhibitors are assembled from one or two heavy chains (H1, H2 or H3) and one light chain, bikunin. Inter-alpha-inhibitor (I-ALPHA-I) is composed of H1, H2 and bikunin, inter-alpha-like inhibitor (I-ALPHA-I) of H2 and bikunin, and pre-alpha-like inhibitor (I-ALPHA-LI) of H3 and bikunin, and pre-alpha-inhibitor (P-ALPHA-I) of H3 and bikunin (By
                                                                                                                                                                                                                                      284
                                                                                                                                                                                                                                                                 69 TGDLATSRNAADSSVPSAPRRQDSEDHSSDMFNYEEYCTANAVTGPCRASFPRWYFDVER 128
                                                                                                                                                                                                                                                                                                                                                                                                                                 AMBP_MERUN STANDARD; PRT; 346 AA.
062577; 062576;
01-NOV-1997 (Rel. 35, Created)
16-OCT-2001 (Rel. 40, Last sequence update)
16-OCT-2001 (Rel. 40, Last annotation update)
AMBP protein precursor [Contains: Alpha-1-microglobulin; Inter-alpha-trypsin inhibitor light chain (ITI-LC) (Bikunin) (HI-30)].
                                                                                                                                                                           Gaps
                                                                                                                                                                                                      9 DFCLVSKVVGRCRASMPRWWYNVTDGSCQLFVYGGCDGNSNNYLTKEECLKKCATVTENA 68
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             yellow chromophore (By similarity).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PTM: Alpha-1-microglobulin contains a covalently linked brown-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   MEDLINE-95110820; PubMed-7529051; dide H., Itoh H., Nawa Y.; "Sequencing of CDNa Profile alpha 1-microglobulin/Dikunin of Mongolian gerbil and Syrian golden hamster in comparison with man
                                                                                                                                                                                                                      229 DSCQLDYSQGPCLGLFKRYFYNGTSMACETFLYGGCMGNUFLSEKECLQTCRTV---
                                                                                                                                                                                                                                                                                                ------EACNLPIVQGPCRSYIQLWAFDAVK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Meriones unguiculatus (Mongolian jird).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Gerbillinae;
                                                                                                                                                                         39;
                                                                                                                                           26.3%; Score 249.5; DB 1; Length 352; 32.4%; Pred. No. 1.3e-16;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PTM: THE PRECURSOR IS PROTEOLYTICALLY PROCESSED INTO TWO SEPARATELY FUNCTIONING PROTEINS.
 T -> G (IN REF. 4).
A -> D (IN REF. 4).
G -> L (IN REF. 2 AND 3).
E -> Q (IN REF. 2 AND 3).
SY -> AF (IN REF. 2 AND 3).
SY -> AF (IN REF. 2 AND 3).
E -> Q (IN REF. 2 AND 3).
E -> R (IN REF. 2 AND 3).
                                                                                                                                                                         Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        -1- SIMILARITY: CONTAINS 2 BPTI/KUNITZ INHIBITOR DOMAINS
                                                                                                            ED31C5CA02E70B19 CRC64;
                                                                                                                                                                         45;
                                                                                                                                                           Pred. No. 1.3e
16; Mismatches
                                                                                                                                                                                                                                                                                                                             129 NSCNNFIYGGCRGNKNSYRSEEACMLRC 156
                                                                                                                                                                                                                                                                                                                                              310 GKCVRFSYGGCKGNGNKFYSEKECKEYC 337
                                                                                                              MW;
                                                                                                            39235
                                                                                                                                                                         Conservative
                217
268
274
2299
330
346
                                              274
298
330
346
352 AA;
                                                                                                                                                        Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          NCBI_TaxID=10047;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   similarity).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TISSUE-Liver;
                                                                                                                                                                         48;
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CONFLICT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TFPI_RAT STANDARD; PRT; 302 AA.

002445.
01-JUL-1993 (Rel. 26, Last sequence update)
01-JUL-1993 (Rel. 26, Last sequence update)
16-OCT-2001 (Rel. 40, Last annotation update)
17:Ssue factor pathway inhibitor precursor (TFPI) (Lipoprotein-associated coagulation inhibitor) (LACI) (Extrinsic pathway inhibitor)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       69 TGDLATSRNAADSSVPSAPRRQDSEDHSSDMFNYEEYCTANAVTGPCRASFPRWYFDVER 128
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               --CNLPIVOGPCRAYIKLWAFDAAQ 308
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             DFCLVSKVVGRCRASMPRWWYNVTDGSCQLFVYGGCDGNSNNYLTKEECLKKCATVTENA 68
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    BYTYKUNITE INHIBIOR 2.
CHROMOPHORE (BY SIMILARITY).
BY SIMILARITY.
                                                                                                                                                                                                                                                                                                                                                               PROSITE; PS00280; BPTI_KUNITZ_1; 2.
PROSITE; PS50279; BPTI_KUNITZ_2; 2.
Glycoprotein; Plasma; Signal; Serine protease inhibitor; Repeat;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           LIGHT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               39;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ELASTASE) (BY SIMILARITY).
INHIBITORY SITE (P1) (TRYPSIN) (BY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ; Score 247.5; DB 1; Length 346;
; Pred. No. 2e-16;
15; Mismatches 46; Indels 39;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           INTER-ALPHA-TRYPSIN INHIBITOR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        F1A4463810918D5F CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      BPTI/KUNITZ INHIBITOR 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                              BY SIMILARITY.
ALPHA-1 MICROGLOBULIN.
                                                                                          or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SIMILARITY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Interpro; IPR00223; Kunitz_BPTI.
InterPro; IPR002345; Lipocalin.
InterPro; IPR000566; Lipocin_cytFABP.
Pfam; PF00014; Kunitz_BPTI; 2.
Pfam; PF00061; lipocalin; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            129 NSCNNFIYGGCRGNKNSYRSEEACMLRC 156
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        38643 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  26.1%;
                                                                                                                                       EMBL; D31813; BAA06600.1; -.
                                                                                                                                                                                                                                                                                               PRINTS; PR00759; BASICPTASE.
PRINTS; PR00179; LIPOCALIN.
SMART; SM00131; KU; 2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          32.4%;
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nes 48; Conservative
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336
52
187
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2263
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205
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2286
249
249
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                                                                                                                                                                                                                                                                                                                                                                                                                                         Lipocalin.
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REDLINES-90105540; PubMed=2481505;
Rasp G., Hochstrasser K., Gerl C., Machter E.;
Rasp G., Hochstrasser K., Gerl C., Machter E.;
Inter-alpha-trypsin inhibitor.
Inter-alpha-trypsin inhibitor.
Inter-alpha-trypsin inhibitor.
Inter-alpha-trypsin inhibitor.
Is blochim. Blophys. Acta 999:335-337(1989).
Inter-alpha-trypsin inhibitor.
Inter-alpha-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Rasp G., Hochstrasser K., Wachter E., Reisinger P.W.M.; "The amino-acid sequence of the trypsin-released inhibitor from sheep inter-alpha-trypsin inhibitor."; Biol. Chem. Hoppe-Seyler 368:727-731(1987).
 --WCLEPADSGLCKA 233
                                                                                                                                                                                                                     01-JAN-1990 (Rel. 13, Last sequence update)
16-OCT-2001 (Rel. 40, Last annotation update)
Inter-alpha-trypsin inhibitor (ITI) (GIK-14) (Inhibitory fragment of
                                                                                                                                                                                                                                                                                                                         Eukaryota: Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovoidea; Bovidae; Caprinae; Ovis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             INHIBITORY SITE (P1) (CHYMOTRYPSIN,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         25.8%; Score 244.5; DB 1; Length 123;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               INHIBITORY SITE (P1) (TRYPSIN).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Plasma; Glycoprotein; Serine protease inhibitor; Repeat. NON_TER 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             BPTI/KUNITZ INHIBITOR 1.
BPTI/KUNITZ INHIBITOR 2.
BY SIMILARITY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     295038173F22D2D1 CRC64;
 182 QKGDYVTNQITVTDRTTVNNVVIPQAŢKAPSQWDYDGPS----
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                                                        SFPRWYFDVERNSCNNFIYGGCRGNKNSYRSEEACMLRC
                                                                                                                                                                  123 AA.
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Pfam; PF00114; Kunitz_BPTI; 2.
SMART; SM00131; KU; 2.
PROSITE; PS00280; BPTI_KUNITZ_1; 2.
PROSITE; PS50279; BPTI_KUNITZ_2; 2.
                                                                                                                                                                                                                                                                                                                                                                                                                                         SPECIES=Sheep;
MEDLINE=87299012; PubMed=2441725;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             72 IN
24 N-
123
13686 MW;
                                                                                                                                                                                                  01-JAN-1990 (Rel. 13, Created)
01-JAN-1990 (Rel. 13, Last seq
16-OCT-2001 (Rel. 40, Last anno
                                                                                                                                                                  STANDARD;
                                                                                                                                                                                                                                                                          ITI) (Fragment).
Ovis aries (Sheep), and
Capra hircus (Goat).
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24
123
123 AA;
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                                                                                                                                                                  IATR_SHEEP
P13371;
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SEQUENCE
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                                                                                                                                               IATR_SHEEP
                                     118
                                                                                                                              RESULT 9
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                                                                                                                                                                  This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                      J. BLOCHEM. 111:681-687(1992).
-!- FUNCTION: INHIBITS FACTOR X (X(A)) DIRECTLY AND, IN A XA-DEPENDENT., WAY, INHIBITS VII(A)/TISSUE FACTOR ACTIVITY, PRESUMABLY BY FORMING A QUAPERNARY X(A)/LAOLYVII(A)/TE COMPLEX. IT POSSESSES AN ANTITHROMBOTIC ACTION AND ALSO THE ABILLITY TO ASSOCIATE WITH
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ----NAADSSVPSAPRRQDSEDHSSDMFNYEEYCTANAVTGPCRA 117
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REACTIVE BOND (BY SIMILARITY).

BY SIMILARITY.

BY SIMILARITY.

BY SIMILARITY.

BY SIMILARITY.

REACTIVE BOND (BY SIMILARITY).

N-LINKED (GLCNAC. .) (POTENTIAL).

N-LINKED (GLCNAC. .) (POTENTIAL).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PRINTS: PRO0759; BASICPTASE.
SMART: SMO0131; KU; 3.
SMART: SMO0131; KU; 3.
PROSTIE: PS00280; BPTI KUNTZ_1; 3.
PROSTIE; PS50279; BPTI KUNITZ_2; 3.
Serine protease inhibitor; Glycoprotein; Repeat; Blood coagulation;
                                                                                      Enjyoji K.-I., Emi M., Mukai T., Kato H.; "cDNA cloning and expression of rat tissue factor pathway inhibitor
                                                                                                                                                                                                                                  LIPOPROTEINS IN PLASMA.
SUBCELLULAR LOCATION: Secreted.
TISSUE SPECIFICITY: MOST ABUNDANT IN HEART, LUNG, KIDNEY, AND AORTIC ENDOTHELLAL CELLS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TISSUE FACTOR PATHWAY INHIBITOR.
BPIL/KUNITZ INHIBITOR 1
(VII(A)/TISSUE FACTOR BINDING SITE).
BPIL/KUNITZ INHIBITOR 2
                                                                                                                                                                                                                                                                                                          DOMAIN: THIS INHIBITOR CONTAINS THREE INHIBITORY DOMAINS. SIMILARITY: CONTAINS 3 BPTI/KUNITZ INHIBITOR DOMAINS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       26.0%; Score 246.5; DB 1; Length 302; 34.0%; Pred. No. 2.2e-16;
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REACTIVE BOND (BY SIMILARITY).
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BPI/KUNITZ INHIBITOR 3.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           21; Mismatches
                                                   STRAIN-SPRAGUE-DAWLEY; TISSUE=Liver;
                                                                     MEDLINE=92348361; PubMed=1639767;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    InterPro; IPR002223; Kunitz_BPTI.
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34554 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           EMBL; D10926; BAA01724.1; -.
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302
103
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261
302 AA;
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les 54; Conserv
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HSSP; P10646
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                                                          DFCLVSKVVGRCRASMPRWWYNVTDGSCQLFVYGGCDGNSNNYLTKEECLKKCATVTENA 68
                                                                                                                                                                                    83
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Inter-alpha
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Traboni C., Cortese R.; "Sequence of a full length cDNA coding for human protein HC (alpha microglobulin).";
                                                                                                                                                                                                                                                                                                                                                                  P02760; P02759; P00977;
21-JUL-1986 (Rel. 01, Created)
13-AUG-1987 (Rel. 05, Last sequence update)
16-OCT-2001 (Rel. 40, Last annotation update)
16-OCT-2form precursor [Contains: Alpha-1-microglobulin (Protein FCOMplex-forming glycoprotein heterogeneous in charge); Inter-alph trypsin inhibitor light chain (ITI-LC) (Bikunin) (HI-30)].
                                                                                 3 DSCQLGYSQGPCLGMFKRYFYNGTSMACETFYYGGCMGNGNNFPSEKECLQTCRTV---
                                                                                                                                                                                  -- OACNLPIVRGPCRAGIELWAFDAVK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Euteleostomi;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            "Structural analysis of the human inter-alpha-trypsin inhibitor
                       39;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             "Structure of the human alpha 1-microglobulin-bikunin gene.";
Biol. Chem. Hoppe-Seyler 371:1185-1196(1990).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Diarra-Mehrpour M., Bourguignon J., Sesboue R., Salier J.P., Leveillard T., Martin J.P.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SEQUENCE OF 20-202 (INDIVIDUAL WITH TUBULAR PROTEINURIA). MEDLINE-84126849; PubMed-6198962; Depez C., Grubb A.O., Mendez E.; "The complete amino acid sequence of human complex-forming 91ycoprotein heterogeneous in charge (protein HC) from one
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Eutele
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo
                       Indels
                47;
  No. 1.2e-16;
                    Mismatches
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  Pred.
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MEDLINE=90336621; PubMed=1696200;
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31.8%;
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                    Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Vetr H., Gebhard W.;
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  Best Local Similarity
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Relatinger P., Hochstrasser K., Albrecht G.J., Lempart K., Salier J.P., "Human inter-alpha-trypsin inhibitor: localization of the Kunitz-type domains in the Nterminal part of the molecule and their release by a trypsin-like proteinase.";
Biol. Chem. Hoppe-Seyler 366:479-483(1985).
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MEDLINE-82074265; PubMed-6171497;
Hochstrasser K., Schoenberger O.L., Rossmanith I., Wachter E.;
Hochstrasser K., Schoenberger inhibitors derived by limited proteolysis of the inter-alpha-trypsin inhibitor, V. Attachments of carbohydrates in the human urinary trypsin inhibitor isolated by affinity
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MEDLINE-91093267; PubMed=1889736;
Enghild J.J., Salvesen G., Hefta S.A., Thoegersen I.B.,
Rutherfurd S., Pizzo S.V.;
"Chondroitin 4-sulfate covalently cross-links the chains of the human
protein HC displays variability in its carboxyl-terminal amino
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Morii M., Travis J.; "The reactive site of human inter-alpha-trypsin inhibitor is in the amino-terminal half of the protein.";
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Escribano J., Lopex-Otin C., Hjerpe A., Grubb A.O., Mendez E.;
"Location and characterization of the three carbohydrate prosthetic
groups of human protein H.C.";
FEBS Lett. 266:167-170(1990).
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MEDLINE-94229087; PubMed-7513643;
Morelle W., Capon C., Balduyck M., Sautiere P., Kouach M.,
Michalski C., Fournet B., Mizon J.;
"Chondroitin sulphae covalently cross-links the three polypeptide chains of inter-alpha-trypsin inhibitor.";
Eur. J. Blochem. 221:881-888(1994).
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                                                                                                                                                             SEQUENCE OF 20-198 (PATIENTS WITH TUBULAR PROTEINURIA). MEDLINE-81184038; PubMed-6164372; Takagi T., Takagi K., Kawai T.; "Complete amino acid sequence of human alpha 1-microglobulin."; Biochem. Biophys. Res. Commun. 98:997-1001(1981).
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MEDLINE-93232026; PubMed-7682553;
Enghild J.J., Salvesen G., Thoegersen I.B., Valnickova Z., Pizzo S.V., Hefta S.A.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Hoppe-Seyler's Z. Physiol. Chem. 362:1357-1362(1981).
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MEDLINE-85225968; PubMed-2408638;
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MEDLINE=91340714; PubMed=1714898;
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                                                 acid sequence.";
FEBS Lett. 144:349-353(1982).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      INHIBITORY SITE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      chromatography
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                                                                                                                                                                                                                                                                                                 SUBUNIT: I ALPHA-I plasma protease inhibitors are assembled from one or two heavy chains (H1, H2 or H3) and one light chain, bikunin. Inter-alpha-inhibitor (I-ALPHA-I) is composed of H1, H2 and bikunin, inter-alpha-like inhibitor (I-ALPHA-LI) of H2 and bikunin, and pre-alpha-inhibitor (P-ALPHA-I) of H3 and bikunin (By
                                             X-RAY CRYSTALLOGRAPHY (2.5 ANGSTROMS) OF 230-339.
MEDLINE-8822731; Pubmed-9566199;
Xu Y., Carr P.D., Guss J.M., Ollis D.L.;
"The crystal structure of bikunin from the inter-alpha-inhibitor complex: a serine protease inhibitor with two Kunitz domains.";
J. Mol. Biol. 276:955-966(1998).
-!- FUNCTION: ALPHA-1-MICROGLOBULIN OCCURS IN MANY PHYSIOLOGICAL FLUNCTION: ALPHA-1-MICROGLOBULIN OCCURS IN MANY PHYSIOLOGICAL FLUNDS INCLUDING PLABMA, URINE, AND CERBEROSPINAL FLUID. IT
APPEARS. NOT ONLY AS A FREE MONOMER BUT ALSO IN COMPLEXES WITH IGA
                                                                                                                                                                                                                FUNCTION: INTER-ALPHA-TRYPSIN INHIBITOR, PRESENT IN PLASMA AND URINE, INHIBITS TRYPSIN, PLASMIN, AND LYSOSOMAL GRANULOCYTIC ELASTARE. ADDITIONAL PROTEOLYTIC PROCESSING IN THE KIDNEY AND/OR URINE CAN PRODUCE FURTHER AMINO- AND CARBOXYL-END MODIFICATIONS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CROSS-LINKING BETWEEN THE DIFFERENT COMPONENTS.
-!- MISCELLANEOUS: IN VITRO, THE FIRST TWENU'R RESIDUES OF THE AMINO END OF THE INHIBITION APPEAR TO HAVE A REACTIVE SITE CAPABLE OF INHIBITING THE ACTIVITY OF A NUMBER OF ENZYMES. ITS IN VIVO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            FUNCTION IS NOT KNOWN. SECTION; BELONGS TO THE LIPOCALIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      -!- PTM: ADDITION OF GLYCOSAMINOGLYCAN CHONDROITIN SULFATE, ALLOWS
                                                                                                                                                                                                                                                                                                                                                                                                                                        PTM: Alpha-1-microglobulin contains a covalently linked brownyellow chromophore.
                                                                                                                                                                                                                                                                                                                                                                                                       PIM: THE PRECURSOR IS PROTEOLYTICALLY PROCESSED INTO TWO SEPARATELY FUNCTIONING PROTEINS.
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InterPro: IPR002345; Lipocalin.
InterPro: IPR003565; Lipocalin.
PF00014; Kunitz_BPTI; 2.
Pfam; PF00061; Lipocalin, 1.
ood protein pre-alpha-inhibitor.";
Biol. Chem. 266:747-751(1991).
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AAA59196.1;
AAA59196.1;
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                                                                                                                                                                                                    AND ALBUMIN
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S13433; S
S10717;
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SWISS-2DPAGE;
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Tissue factor pathway inhibitor precursor (TFPI) (Lipoprotein-
associated coagulation inhibitor) (LACI) (Extrinsic pathway inhibitor)
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"Revised oDNA sequence of rabbit tissue factor pathway inhibitor.";
Thromb. Res. 69:547-553(199).
-!- FUNCTION: INHIBITS FACTOR X (X(A)) DIRECTLY AND, IN A XA-DEPENDENT
WAY, INHIBITS VIIIAA/TISSUE RACTOR ACTIVITY, PRESUMABLY BY FORMING
A QUATERNARY X(A)/LACI/VII(A)/TF COMPLEX. IT POSSESSES AN
ANTITHROMBOTIC ACTION AND ALSO THE ABILITY TO ASSOCIATE WITH
                                                                                                                                                                                                                                                                                     --CNLPIVRGPCRAFIQLWAFDAVK 309
                                                                                                                                                                                                                                                69 TGDLATSRNAADSSVPSAPRQDSEDHSSDMFNYEEYCTANAVTGPCRASFPRWYFDVER 128
                                                                 Gaps
                                                                                                                          9 DFCLVSKVVGRCRASMPRWWYNVTDGSCQLEVYGGCDGNSNNYLTKEECLKKCATVTENA 68
                                                                                                                                                              229 DSCQLGYSAGPCMGMTSRYFYNGTSMACETFQYGGCMGNGNNFVTEKECLQTCRTVAA--
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Lagomorpha; Leporidae; Oryctolagus.
                                                              39;
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-!- SUBCELLULAR LOCATION: Secreted.
-!- DOMAIN: THIS INHIBITOR CONTAINS THREE INHIBITORY DOMAINS.
-!- SIMILARITY: CONTAINS 3 BPTI/KUNITZ INHIBITOR DOMAINS.
   Length 352;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Wesselschmidt R.L., Girard T.J., Broze G.J. Jr.; "CDNA sequence of rabbit lipoprotein-associated coagulation inhibitor.";
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DB 1;
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                             4e-16;
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                                                              Mismatches
Score 244.5;
Pred. No. 4e-
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EMBL; S61902; AAB26836.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   MEDLINE=92335027; PubMed=1630940;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   MEDLINE=91057146; PubMed=2136251;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                MEDLINE=93276427; PubMed=8503123;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            | TRABIT | STAND. | TFPI RABIT | STAND. | 19761; Q28828; | 01-FEB-1991 (Rel. 17, Created) | 01-FEB-1992 (Rel. 23, Last seque | 01-AUG-1992 (Rel. 40, Last annot more annotation | mathway inhibitor | mathway 
                                                           14;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        REVISIONS TO 72; 211 AND 218
25.8%;
                                                              Conservative
                             Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            NCBI_TaxID=9986;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TISSUE-Liver;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TISSUE-Lung;
                                                              48;
Query Match
Best Local (
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                                                           Matches
                                                                                                                                                                                                                                                                                                               287
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3.5

T.

us-09-218-913d-52.rsp

amino acid sequences of procine alpha

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NON_TER
SIGNAL
CHAIN
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BINDING
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CHAIN
5
                                                                                                                                                                                                                                                                                                                                                               64 VTENATGDLATSRNAADSSVPSAPRRQDSEDHSSDMFNYEEYCTANAVTGPCRASFPRWY 123
                                                                                                                                                                                                                                                                                                                                                                                                         103 DYPKMTTKLTFQKGKPD---------FCFLEEDPGICKGYITRYF 138
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   AMBP_PIG STANDARD; PRT; 337 AA.
P04356; P34954;
20-MAR-1997 (Rel. 04, Created)
01-FEB-1994 (Rel. 28, Last sequence update)
16-OCT-2001 (Rel. 40, Last annotation update)
4-Coct-2001 (Rel. 40, Last annotation update)
trypsin inhibitor light chain (ITI-LC) (Bikunin) (HI-30) (EI-14)]
                                                                                                                                                                                                                                                                                                                                       Gaps
                                                                                                                                                                                                                                                                                                                                                      4 ERSIHDFCLVSKVVGRCRASMPRWWYNVTDGSCQLFVYGGCDGNSNNYLTKEECLKKCAT 63
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 MEDLINE-90353595; PubMed-1696914;
Gebhard W., Schreitmueller T., Vetr H., Wachter E., Hochstrasser K.;
                                               PROSITE: PS10280; BPTI_KUNITZ_1; 3.
PROSITE; PS50279; BPTI_KUNITZ_2; 3.
Serine protease inhibitor; Glycoprotein; Repeat; Blood coagulation;
                                                                                                                                                                                                                                       BY SIMILARITY.

REACTIVE BOND (BY SIMILARITY).

N-LINKED (GLCNAC. . .) (POTENTIAL).

MISSING (IN REF. 3).

PKSI -> RNLS (IN REF. 3).

AM. AOBDE36537708CA6 CRC64;
                                                                                                  BPTI/KUNITZ INHIBITOR I
(VII(A)/TISSUE FACTOR BINDING SITE).
BPTI/KUNITZ INHIBITOR 2
(FACTOR X(A) BINDING SITE).
BPTI/KUNITZ INHIBITOR 3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Euteleostomi;
Sus.
                                                                                                                                                                                                                                                                                                                                     28;
                                                                                            TISSUE FACTOR PATHWAY INHIBITOR.
                                                                                                                                                     BY SIMILARITY.
BY SIMILARITY.
BY SIMILARITY.
REACTIVE BOND (BY SIMILARITY).
BY SIMILARITY.
BY SIMILARITY.
BY SIMILARITY.
BY SIMILARITY.
REACTIVE BOND (BY SIMILARITY).
                                                                                                                                                                                                                                                                                                                    Length 300;
                                                                                                                                                                                                                                                                                                                    25.7%; Score 244; DB 1; Length 30 llarity 30.0%; Pred. No. 3.7e-16; Conservative 23; Mismatches 61; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sus scrofa (Pig).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata;
Mammalia; Eutheria; Cetartiodactyla; Suina; Suidae;
                                                                                                                                                                                                                                                                                                                                                                                                                          124 FDVERNSCNNFIYGGCRGNKNSYRSEEACMLRCFRQQENP 163
                                                                                                                                                                                                                                                                                                                                                                                                                                   139 YNNQSKQCERFKYGGCLGNLNNFESLEECKNTC---ENP 174
                                                                                                                                              (BY SIMILARITY).
                                                                                                                                                                                                                         SIMILARITY.
       HSSP; P10646; 1TFX.
InterPro; IPR002223; Kunitz_BPTI.
                                                                                                                                                                                                                         BY
BY
BY
                                                                                                                                                                                                                                                                                                    34435 MW;
                       Pfam; PF00014; Kunitz_BPTI;
PRINTS; PR00759; BASICPTASE.
SMART; SM00131; KU; 3.
                                                                                   24
300
100
                                                                                                                                                      171
                                                                                                                                    263
                                                                                                                                                                                                                                                                                    31
269
300 AA;
                                                                                                                                                                                                                                                                                                                             Local Similarity
nes 48; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SEQUENCE FROM N.A.
                                                                                     1
25
50
                                                                                                                                    213
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                                                                                                                     121
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               (Fragment).
AMBP OR ITIL.
                                                                                                                                                              DISULFID
                                                                                                                                                                               ACT_SITE
DISULFID
                                                                                                                                                                                                        DISULFID
ACT_SITE
                                                                                                                                                                                                                                DISULFID
                                                                                                                                                                                                                                                                                           CONFLICT
                                                                                                                                                      DISULFID
                                                                                                                                                                                                 DISULFID
                                                                                                                                                                                                                          DISULFID
                                                                                                                                                                                                                                                   ACT_SITE
                                                                                                                                                                                                                                                            CARBOHYD
                                                                                                                                                                                                                                                                    CARBOHYD
                                                                                                                                                                                                                                                                            CARBOHYD
                                                                                                                                                                                                                                                                                                                     Query Match
                                                                                    SIGNAL
                                                                                                                    DOMAIN
                                                                                                    DOMAIN
                                                                                                                                     DOMAIN
                                                                             Siqnal
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                     RESULT 12
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This SWISS-PROT entry is copyright. It is produced through a collaboration. between the Swiss Institute of Bioinformatics and the EMBL outstation - the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (see http://www.isb-sib.ch/announce.or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SUBBUNIT: I-ALPHA-I plasma protease inhibitors are assembled from one or two heavy chains (H1, H2 or H3) and one light chain, blunin. Inter-alpha-inhibitor (I-ALPHA-I) is composed of H1, H2 and bikunin, inter-alpha-like inhibitor (I-ALPHA-LI) of H2 and bikunin, and pre-alpha-inhibitor (P-ALPHA-I) of H3 and bikunin (By
                                                                                                                                                                                                                                                                                                                                                                                    "Molecular cloning of porcine alpha 1-microglobulin/HI-30 reveals developmental and tissue-specific expression of two variant messenger
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        yellow chromophore.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              FUNCTION: INTER-ALPHA-TRYPSIN INHIBITOR, PRESENT IN PLASMA AND URINE, INHIBITS TRYPSIN, PLASMIN, AND LYSOSOMAL GRANULOCYTIC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SEPARATELY FUNCTIONING PROTEINS.
-!- PTM: Alpha-1-microglobulin contains a covalently linked brown-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Glycoprotein; Plasma; Signal; Serine protease inhibitor; Repeat; Lipocalin.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            INTER-ALPHA-TRYPSIN INHIBITOR LIGHT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PTM: THE PRECURSOR IS PROTEOLYTICALLY PROCESSED INTO TWO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      -!- SIMILARITY: CONTAINS 2 BPTI/KUNITZ INHIBITOR DOMAINS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CHAIN.

BPTI/KUNITZ INHIBITOR 1.
BPTI/KUNITZ INHIBITOR 2.
CHROMOPHORE (BY SIMILARITY).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     BY SIMILARITY.
ALPHA-1-MICROGLOBULIN.
                                                                                                                                                                                                                                                                                                    Biochim. Biophys. Acta 1088:47-56(1991).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             EMBL, X53685; CAA37725.1; -.
EMBL; X2087; CAA36306.1; -.
PIR; A010208; TIPGBI.
PIR; S11066; S11066.
HSSP; P02760; 1BIK.
InterPro; IPR002223; Kunitz_BPTI.
InterPro; IPR002223; Kunitz_BPTI.
Pfam; PF00014; Kunitz_BPTI.
Pfam; PF00061; lipocalin; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PROSITE; PS00280; BPTI_KUNITZ_1; 2.
PROSITE; PS50279; BPTI_KUNITZ_2; 2.
                                                                                                                                       TISSUE=Liver;
MEDLINE=91113729; PubMed=1703444;
"Complementary DNA and deduced 1-microglobulin and bikunin."; FEBS Lett. 269:32-36(1990).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PROSITE; PS00213; LIPOCALIN;
                                                                                                             SEQUENCE OF 2-337 FROM N.A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             266
322
38
                                                                                                                                                                                                                                                                                                                                                                SEQUENCE OF 212-334.
                                                                                                                                                                                                                                                                               ribonucleic acids."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          AND ALBUMIN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 191
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             216
272
38
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          similarity)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ₽
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ELASTASE.
                                                                                                                                                                                           Tavakkol A.;
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HSSP; P02760; 1BIK
                                                                                                                                                                                                                                                                                                                 Matches
                                                                                                                                                                                                                                                                                                                                                                                                                    61
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Hochstrasser K., Wachter E., Albrecht G.J., Reisinger P.;
"Kunitz-type proteinase inhibitors derived by limited proteolysis of
the inter-alpha-trypsin inhibitor. X. The amino-acid sequences of the
trypsin-released inhibitors from horse and pig inter-alpha-trypsin;
inhibitors.";
Biol. Chem. Hoppe-Seyler 366:473-478(1985).

FUNCTION: THIS INHIBITORY FRAGMENT, RELEASED FROM NATIVE ITI AFFER
LIMITED PROFEDLYSIS WITH TRYPSIN, CONTAINS TWO HOWOLOGUES DOWAINS.
WHEREAS THE SECOND DOMAIN IS A STRONG INHIBITOR OF TRYPSIN, THE
                                                                                                                                                                                                                                                                                                                                                       FIRST DOMAIN INTERACTS WEAKLY WITH PON-GRANULOCYTIC ELASTASE AND NOT AT ALL WITH PANCREATIC ELASTASE.

MISCELLANBOUS: THE AMINO ACID AT POSITION P2' (17) APPEARS TO DETERMINE THE SPECIFICITY OF THE INHIBITION OF DOMAIN I.

INHIBITORS WITH METHIONINE IN THIS POSITION INTERACT WEAKLY WITH GLYMOPREPSIN AND ELASTASE; THOSE WITH LEUCINE INTERACT STRONGLY.

SIMILARITY: CONTAINS 2 BPTI/KUNITZ INHIBITOR DOMAINS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      20-MAR-1987 (Rel. 04, Created)
20-MAR-1987 (Rel. 04, Last sequence update)
16-OCT-2001 (Rel. 40, Last annotation update)
Inter-alpha-trypsin inhibitor (ITI) (HI-14) (Inhibitory fragment of
                                                                                                                                                                                                                                                                                                                                                                                         TGDLATSRNAADSSVPSAPRQDSEDHSSDMFNYEEYCTANAVTGPCRASFPRWYFDVER
                                                                                                                                                                                                                                                                                                                                                                                                                DFCLVSKVVGRCRASMPRWWYNVTDGSCQLFVYGGCDGNSNNYLTKEECLKKCATVTENA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Vertebrata; Euteleostomi;
                                                                                        N-LINKED (GLCNAC. . .) (POTENTIAL).
                                                                                                                INHIBITORY SITE (P1) (CHYMOTRYPSIN,
                                                                                                                                  INHIBITORY SITE (P1) (TRYPSIN).

T -> M (IN REF. 2).

E -> Q (IN REF. 3).

S -> Q (IN REF. 3).

G -> A (IN REF. 3).

FQ -> IR (IN REF. 3).

V -> A (IN REF. 3).

V -> A (IN REF. 3).

W -> A (IN REF. 3).

E -> Q (IN REF. 3).

E -> Q (IN REF. 3).
                                                                                                                                                                                                                                                                                         DB 1; Length 337;
                                                                                                                                                                                                                                                                                                                 Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Eukaryota; Metazoa; Chordata; Craniata; Vertebrata;
Mammalia; Eutheria; Perissodactyla; Equidae; Equus.
                                                                                                                                                                                                                                                                                       Score 242.5; DB 1
Pred. No. 5.9e-16;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                123 AA
  SIMILARITY
                                                                                                                                                                                                                                                                                                                 Mismatches
                                                                                                                           ELASTASE)
                                                                                                                                                                                                                                                                                                                                                                                                                                                        295 GKCVLFNYGGCQGNGNQFYSEKECKEYC 322
                                                                                                                                                                                                                                                                                                                                                                                                                                          129 NSCNNFIYGGCRGNKNSYRSEEACMLRC 156
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SEQUENCE.
MEDLINE=85225967; PubMed=2408637;
                                                                                                                                                                                                                                                                                                                19;
                                                                                                                                                                                                                                                               37690 MW;
                                                                                                                                                                                                                                                                                       25.6%;
31.8%;
                                                                                                                                                                                                                                                                                                                 Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                STANDARD;
                                                                                                                                                  49
259
270
278
278
286
293
311
315
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Equus caballus (Horse)
                                                                                                                                                                                                                                                                 AA;
                                                                                                                                                                                                                                                                                       Query Match
Best Local Similarity
Matches 47; Conserv
                                                                                                                                                                                                                        293
311
315
337 I
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     NCBI_TaxID=9796;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ITI) (Fragment)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              IATR_HORSE
P04365;
DISULFID
DISULFID
DISULFID
DISULFID
DISULFID
                                                                                                                                                                                                            CONFLICT
CONFLICT
CONFLICT
CONFLICT
SEQUENCE
                                                            DISULFID
                                                                                                                                      ACT_SITE
CONFLICT
                                                                                      CARBOHYD
                                                                                                     CARBOHYD
                                                                                                                ACT_SITE
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Kastern W., Bjoerck L., Aakerstroem B.; "Developmental and tissue-specific expression of alpha 1-microglobulin mRNA in the rat.";
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01-FEB1-1991 (Rel. 17, Created)

01-NOV-1997 (Rel. 35, Last sequence update)

16-OCT-2001 (Rel. 40, Last annotation update)

16-OCT-2010 (Rel. 40, Last annotation update)

16-OCT-2010 (Rel. 40, Last annotation update)

16-OCT-2011 (Rel
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       69 TGDLATSRNAADSSVPSAPRRQDSEDHSSDMFNYEEYCTANAVTGPCRASFPRWYFDVER 128
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 9 DFCLVSKVVGRCRASMPRWWYNVTDGSCQLFVYGGCDGNSNNYLTKEECLKKCATVTENA 68
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ------CNLPIVQGPCRAFIRLWAFDAAQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Lindqvist A., Bratt T., Altieri M., Kastern W., Aakerstroem B.; Rat alpha 1-microglobulin: co-expression in liver with the light chain of inter-alpha-trypsin inhibitor:"; Biochim. Biophys. Acta 1130:63-67(1992).
                                                                                                                                                                                                                                                                                                                                                                                                                                                  INHIBITORY SITE (P1) (CHYMOTRYPSIN,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      39;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              DB 1; Length 123;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             INHIBITORY SITE (P1) (TRYPSIN)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Indels
                                                                          PROSITE; PS00280; BPTLKUNIT2_1; 2.
PROSITE; PS50279; BPTLKUNIT2_2; 2.
Plasma; Glycoprotein; Serine protease inhibitor; Repeat.
NON_TER 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    123
13510 MW; CE1A9120774411D5 CRC64;
                                                                                                                                                                                                            BPTI/KUNITZ INHIBITOR BPTI/KUNITZ INHIBITOR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     N-LINKED (GLCNAC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Score 241.5; DB 1
Pred. No. 2.4e-16;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Mismatches
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STRAIN=WISTAR;
MEDLINE=89053978; Pubmed=3263966;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ELASTASE)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             129 NSCNNFIYGGCRGNKNSYRSEEACMLRC 156
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  GKCVLFTYGGCRGNGNKFYSQKECKEYC 111
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Biol. Chem. 261:15070-15074(1986)
InterPro; IPR002223; Kunitz_BPTI.
Pfam; PF00014; Kunitz_BPTI; 2.
SMART; SM00131; KU; 2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SEQUENCE OF 141-195 FROM N.A. MEDLINE=87033744; Pubmed=2429963;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     MEDLINE=92182014; PubMed=1371936;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      15;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           25.5%;
31.8%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Rattus norvegicus (Rat).
                                                                                                                                                                                                         55
111
55
38
38
51
111
111
107
16
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   23 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Local Similarity
les 47; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE FROM N.A. TISSUE=Liver;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  NCBI_TaxID=10116;
                                                                                                                                                                                                                                                                       5
114
330
61
70
86
                                                                                                                                                                                                                                        DOMAIN
DISULFID
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ACT_SITE
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CARBOHYD
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SEQUENCE
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Best Loca
Matches
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                                                                                                                                                                                                                         URINE, INTER ALERA TRIPOIN INHIBITOR, PRESENT IN PLANMA AND URINE, INHIBITA TRYPOIN.

ELASTASE (BY SIMILARITY). PLASMIN, AND LYSOSOMAL GRANULOCYTIC
ELASTASE (BY SIMILARITY). PLASMIN, AND LYSOSOMAL GRANULOCYTIC
COGGULATION factor Xa and trypsin inhibitor. It inhibits blood
coagulation factor Xa and trypsin and chymase. It is a monomer but
than porcine pancreatic trypsin and chymase. It is a monomer but
is also found in mast cells as a complex with tryptase.
SUBGNIT: I-ALPHA-I plasma protease inhibitors are assembled from
one or two heavy chains (HI, H2 or H3) and one light chain,
bikunin. Inter-alpha-inhibitor (I-ALPHA-I) is composed of H1, H2
and bikunin, incer-alpha-inhibitor (P-ALPHA-I) of H3 and bikunin (By
similarity).
                                                                              MEDLINE-94148892; PubMed=7508921;
Itoh H., Ide H., Ishikawa N., Nawa Y.;
Ishol H., Ishikawa N., Nawa Y.;
J. Biol. Chem. 269:3818-3822(1994).
-!- FUNCTION: ALPHA-1-MICROGLOBULIN OCCURS IN MANY PHYSIOLOGICAL APPEARS NOT ONLY AS A FREE MONOMER BUT ALSO IN COMPLEXES WITH ICA AND ALBUMIN (BY SIMILARITY).
                Kunitz-type protease inhibitor found in rat mast cells. Purification,
                                                                                                                                                                                                                                                                                                                                                                                                     mast cell granules
                                                                                                                                                                                                                                                                                                                                                                                                                PTM: The precursor is proteolytically processed into separately functioning proteins.

Functioning proteins.

FIM: Alpha-1-microglobulin contains a covalently linked brownyellow chromophore (By similarity).

FIM: Heavy chains are interlinked with bikunin via a chondroitin 4-sulfate bridge to the their C-terminal aspartate (By
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    similarity).
SIMILARITY: IN THE N-TERMINAL SECTION; BELONGS TO THE LIPOCALIN
                                                                                                                                                                                                                 FUNCTION: INTER-ALPHA-TRYPSIN INHIBITOR, PRESENT IN PLASMA AND
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 INTER-ALPHA-TRYPSIN INHIBITOR LIGHT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Glycoprotein; Plasma; Signal; Serine protease inhibitor; Repeat;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        INHIBITOR 2. (BY SIMILARITY).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              -! - SIMILARITY: CONTAINS 2 BPTI/KUNITZ INHIBITOR DOMAINS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           INHIBITOR 1.
                                                                                                                                                                                                                                                                                                                                                                                                     present in
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ALPHA-1-MICROGLOBULIN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SIMILARITY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TRYPSTATIN.
BPTI/KUNITZ I
BPTI/KUNITZ I
CHROMOPHORE (
                                                                                                                                                                                                                                                                                                                                                                                                  SUBCELLULAR LOCATION: Trypstatin is
                             operties, and amino acid sequence.";
Biol. Chem. 263:18104-18107(1988).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          nascr. red.co. 1200223; Kunitz_BPTI.
InterPro; IPR002345; Lipocalin.
InterPro; IPR00366; Lipocalin.
Pfam: PF00014; Kunitz_BPTI; 2.
Pfam: PF000611; lipocalin; 1.
Kido H., Yokogoshi Y., Katunuma N.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PROSITE; PS00280; BPTI_KUNITZ_1; 2. PROSITE; PS50279; BPTI_KUNITZ_2; 2. PROSITE; PS00213; LIPOCALIN; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        EMBL; S87544; AAB21782.1; -. EMBL; J02600; AAA41596.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PRINTS; PR00759; BASICPTASE.
PRINTS; PR00179; LIPOCALIN.
SMART; SM00131; KU; 2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            343
280
336
52
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PIR; A31890; A31890.
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230
286
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BINDING
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           DOMAIN
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    -i- FUNCTION: INHIBITS FACTOR X (X(A)) DIRECTLY AND, IN A XA-DEPENDENT WAY, INHIBITS VII(A)/TISSUE FACTOR ACTIVITY, PRESUBABLY BY FORMING A QUATERNARY X(A)/LACI/VII(A)/TF COMPLEX. IT POSSESSES AN ANTITHROMBOTIC ACTION AND ALSO THE ABILITY TO ASSOCIATE WITH
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 associated coagulation inhibitor) (LACI) (Extrinsic pathway inhibitor)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           69 TGDLATSRNAADSSVPSAPRRQDSEDHSSDMFNYEEYCTANAVTGPCRASFPRWYFDVER 128
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     -- CNLPIVQGPCRAFAELWAFDAAQ 308
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            228 DSCQLNYSEGPCLGMQQKYYYNGASMACETFQYGGCLGNGNNFASEKECLQTCRTIAA-- 285
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Kamel S., Kamikubo Y., Hanuro T., Fujimoto H., Ishihara M., Yonemura H., Miyamoto S., Funatsu A., Enjyoji K., Abumiya T.; Amino acid sequence and inhibitory activity of rhesus monkey tissue dactor pathway inhibitor (FFPI): comparison with human TFPI."; J. Biochem. 115:708-714(1994).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                DFCLVSKVVGRCRASMPRWWYNVTDGSCQLFVYGGCDGNSNNYLTKEECLKKCATVTENA 68
BY SIMILARITY.
N-LINKED (GLCNAC. . . ) (POTENTIAL).
N-LINKED (GLCNAC. . . ) (POTENTIAL).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Cercopithecidae;
                                                                                                                                                                                              N-LINKED (GLCNAC. . .) (POTENTIAL) .
INHIBITORY SITE (P1) (CHYMOTRYPSIN,
                                                                                                                                                                                                                                            ELASTASE) (BY SIMILARITY).
INHIBITORY SITE (P1) (TRYPSIN) (BY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   39;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Tissue factor pathway inhibitor precursor (TFPI) (Lipoprotein-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    DB 1; Length 349;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  LIPOPROTEINS IN PLASMA.
--- SUBCELLULAR LOCATION: SECRETEd.
--- DOMAIN: THIS INHIBITOR CONTAINS THREE INHIBITORY DOMAINS.
---- PUTH: O-GLYCOSYLATED (BY SIMILARITY).
---- SIMILARITY: CONTAINS 3 BPTI/KUNITZ INHIBITOR DOMAINS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Indels
                                                                                                                                                                                                                                                                                                                                                                                                             -> W (IN REF. 3).
1B7FB7DCB0824E01 CRC64;
                                                                                                                                                                                                                                                                                      SIMILARITY.
G -> A (IN REF. 2).
W -> L (IN REF. 3).
G -> N (IN REF. 3).
KE -> PR (IN REF. 3).
E -> W (IN REF. 3).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        .8e-15;
les 47;
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(Rel. 38, Last sequence update)
(Rel. 40, Last annotation update)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  25.1%; Score 237.5;
30.4%; Pred. No. 1.8e
ive 17; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               309 GKCIQFIYGGCKGNGNKFYSEKECKEYC 336
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    129 NSCNNFIYGGCRGNKNSYRSEEACMLRC 156
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TISSUE=Liver;
MEDLINE=94375417; PubMed=8089087;
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                                                                                                                                                                                                                                                                                                                 142 G
302 W
323 G
331 K)
334 E
38851 MW;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    6-OCT-2001 (Rel. 40,
                                                                                                                                                                                                                                                                                                                                                                                                             334
349 AA;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       286 -----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    NCBI_TaxID=9544;
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  and the EMBL outstation -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           REACTIVE DOWN.

BY SIMILARITY.

BY SIMILARITY.

BY SIMILARITY.

REACTIVE BOND (BY SIMILARITY).

N'INKED (GLONAC. ..) (POTENTIAL).

N'INKED (GLONAC. ..) (POTENTIAL).
                                                                                                                                                       HSSP; P10646; 1TFX.
InterPro; IPR00223; Kunitz_BPTI.
PFam; PF00014; Kunitz_BPTI; 3.
PRINTS; PR00759; BASICPTASE.
SWART; SW00131; KU; 3.
PROSITE; PS00280; BPTI_KUNITZ_1; 3.
PROSITE; PS0029; BPTI_KUNITZ_2; 3.
Serine protease inhibitor; Glycoprotein; Repeat; Blood coagulation;
                                                                                                                                                                                                                                                                                                                                   BY SIMILARITY.
TISSUE FACTOR PATHWAY INHIBITOR.
BPIL/KUNITZ INHIBITOR 1
(VII(A)/TISSUE FACTOR BINDING SITE).
BPIL/KUNITZ INHIBITOR 2
(FACTOR X(A) BINDING SITE).
BPIL/KUNITZ INHIBITOR 3.
BY SIMILARITY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            BY SIMILARITY.

BY SIMILARITY.

BY SIMILARITY.

REACTIVE BOWD (BY SIMILARITY).
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BY SIMILARITY.
BY SIMILARITY.
REACTIVE BOND (BY SIMILARITY).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match
24.9%; Score 236.5; DB 1; Length
Best Local Similarity 34.9%; Pred. No. 2e-15;
Matches 53; Conservative 24; Mismatches 64; Indels
the Swiss Institute of Bioinformatics
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               145
195
N-
256
N-
35085 MW;
                                                                                                                                    EMBL; S73337; AAB31955.1; -.
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304
104
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29
54
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DISULFID
DISULFID
ACT_SITE
DISULFID
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DISULFID
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CARBOHYD
CARBOHYD
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                                                                                                                                                                                                                                                                                                                    Signal.
SIGNAL
                                                                                                                                                                                                                                                                                                                                                                              DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                   DOMAIN
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9 DFCLVSKVVGRCRASMPRWWYNVTDGSCQLFVYGGCDGNSNNYLTKEECLKKCATVTENA 68

11; Gaps

Length 304;

69 TG----DLATSRNAADSSVPSAPRRQDSEDHSSDMFNYEEYCTANAVTGPCRASFPRWYF 124 q δλ

125 DVERNSCNNFIYGGCRGNKNSYRSEEACMLRC 156 ö

Search completed: October 18, 2002, 10:34:09 Job time : 13 secs

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October 18, 2002, 10:33:48; Search time 17 Seconds (without alignments) 960.893 Million cell updates/sec
5.1.3
Compugen Ltd.
  GenCore version
Copyright (c) 1993 - 2002
                                                                                       OM protein - protein search, using sw model
                                                                                                                                   Run on:
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US-09-218-913D-52 948 1 ADRERSIHDFCLVSKVVGRC......ACMLRCFRQQENPPLPLGSK 170 Perfect score: Sequence:

BLOSUM62 Gapop 10.0 , Gapext 0.5 Scoring table:

283138 Total number of hits satisfying chosen parameters:

283138 seqs, 96089334 residues

Searched:

Minimum DB seq length: 0 Maximum DB seq length: 200000000

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

PIR\_71:\*
1: pir1:\*
2: pir2:\*
3: pir3:\*
1: pir4:\* Database

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

	ription	hepatocyte growth		hypothetical prote	alpha-1-microglobu	tissue factor path	inter-alpha-trypsi	alpha-1-microalobu	tissue factor path	റ	alpha-1-microglobu	alpha-1-microglobu	hypothetical prote	tissue factor path	alpha-1-microdlobu	tissue factor path		tissue factor path	hypothetical prote	hypothetical prote	tissue factor path	J	hypothetical prote				~	hypothetical prote	amyloid precursor	
SUMMARIES	ID	JG0185	C89114	T34395	TIBOBI	TIRTGK	A29652	нсно	146937	S12143	TIPGBI	TIHOBI	T26063	S53325	S21089	JC2264	S35708	TIHUGK	T19734	T23573	A54951	S42880	T26859	A49974	A49321	T16210	H88380	T20406	S41082	D88550
	DB	. 7	7	~	Н	Н	7	7	7	7	Н	7	~	~	7	-	7	_	7	7	7	7	~	7	~	7	7	7	7	7
	4	252	1558	2167	352	302	123	352	299	300	337	125	2225	396	349	304	349	304	1043	922	235	765	1743	751	763	1599	1522	1391	111	1474
ď	Query	69.4	26.4	26.4	26.3	26.0		25.8				25.5							23.4	23.1	22.6	22.2	22.0	21.9	21.1	21.1	21.0	20.6	20.4	20.4
	Score	658	250.5	250.5	249.5	246.5	244.5	244.5	244	243	242.5	241.5	-	239.5	237.5	236.5	235.5	233.5	222	219	214.5	210	209	208	200	200	199		193.5	193
	Result No.	П	2	e	4	5	9	7	8	6	10	11	12	13	14	15	16	17	18	19	20	21	22	23	24	25	26	27	28	29

hypothetical prote	protein ZC84.1 [im	Alzheimer's diseas	hypothetical Alzhe	Alzheimer's diseas	hypothetical prote	gamma-1-microglobu	hypothetical prote	Alzheimer's diseas	Alzheimer's diseas	Alzheimer's diseas	Alzheimer's diseas	hypothetical prote	proteinase inhibit	hypothetical prote	alpha-1-microglobu
S28291	E88550	JH0773	A32761	QRHUA4	T21275	S22181	T33216	803607	S04855	806678	A32282	T32980	S07451	T20125	JC2556
7	7	7	4	-	7	Н	7	7	N	7	7	N	7	7	7
2844	1416	747	484	770	1203	355	1965	97	97	9/	100	692	62	838	372
20.4	20.1	19.7	19.6	19.6	19.6	19.1	18.8	18.5	18.4	18.4	18.4	18.4	17.6	17.3	17.2
193 20.4										174.5 18.4					163.5 17.2

## ALIGNMENTS

RESULT 1

JG0185 hepatcoyte growth factor activator inhibitor type 2 - mouse C;Species: Mus musculus (house mouse) C;Date: 23-Jul-1999 #sequence_revision 23-Jul-1999 #text_change 11-May-2000 C;Date: 23-Jul-1999 #sequence_revision 23-Jul-1999 #text_change 11-May-2000 C;Date: 23-Jul-1999 #sequence_revision 23-Jul-1999 #text_change 11-May-2000 C;Date: 23-Jul-1999 #sequence_revision 25-Jul-1999 #text_change 11-May-2000 C;Date: 23-Jul-1999 #sequence_revision 25-Jul-1999 #text_change 11-May-2000 A;Titoh, H.; Kataoka, H.; Hamasuna, R.; Kitamura, N.; Koono, M. Biochem. Biophys. Res. Commun. 255, 740-748, 1999 A;Titoh, H.; Kataoka, H.; MulD: 99160423 A;Titoh, H.; Kataoka, H.; MulD: 99160423 A;Steference number: JG0185; MUID: 99160423 A;Steference number: JG0185; MUID: 99160423 A;Residues: 1-25 <ito> A;Residues: 1-25 <ito> A;Crossion: JG0185 A;Residues: 1-25 <ito> A;Crossion: JG0185 A;Residues: 1-25 <ito> A;Crossion: JG0185 A;Cross</ito></ito></ito></ito>
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ö Length 252; 34; Indels ; Score 658; DB 2; ; Pred. No. 9.6e-52; 20; Mismatches 34 69.48; 68.28; Query Match
Best Local Similarity 68.28
Matches 116; Conservative

ö

61 CATVTENATGDLATSRNAADSSVPSAPRRQDSEDHSSDMFNYEEYCTANAVTGPCRASFP 120 Gaps 1 ADRERSIHDFCLVSKVVGRCRASMPRWWYNVTDGSCQLFVYGGCDGNSNNYLTKEECLKK 60 q q ò δλ

121 RWYFDVERNSCNNFIYGGCRGNKNSYRSEEACMLRCFRQQENPPLPLGSK 170 δy

protein C37C3.6a [imported] - Caenorhabditis elegans C;Species: Caenorhabditis elegans C;Date: 10-May-2001 #sequence\_revision 10-May-2001 #text\_change 10-May-2001 C;Accession: C89114 RESULT 2 C89114

A status: preliminary

A) Science 283, 2012-2018, 1998

A) Title: Genome sequence of the nematode C. elegans: a platform for investigating bio A) Title: Genome sequence of the nematode C. elegans: a platform for investigating bio A) Riference number: A75000; MUDI:99069613; PMID:9851916

A) Note: published errata appeared in Science 283, 35, 1999; Science 283, 2103, 1999; A) Accession: C89114

A) Science 283, 2103, 1999; A) Science 283, 2103, 1999

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A; Molecule Fype: mRNA
A; Residues: 1-352 <LIN)
A; Cross-references: EMBL:035642; NID:91016297; PIDN:AAB07599.1; PID:91016298
A; Cross-references: EMBL:075642; NID:91016297; PIDN:AAB07599.1; PID:91016298
B; Hochstrasser, K.; Wachter, E.
Hoppe-Seyler's Z. Physiol. Chem. 364, 1679-1687, 1983
A; Title: Kunitz-type proteinase inhibitors derlyed by limited proteolysis of the inte
A; Reference number: A91717; MUID:84133807
                                                                                                                                                                                                                                                                                                                                                    A; Molecule type: protein
A; Residues: 227-267, 'L', 269-273, 'Q', 275-297, 'AF', 300-329, 'Q', 331-345, 'R', 347-348 <HOC
R; Hochstrasser, K.; Machter, E.; Albrecht, G.J.; Reisinger, P.
Biol. Chem. Hoppe-Seyler 366, 473-478, 1985
A; Title: Kunitz-type proteinase inhibitors derived by limited proteolysis of the inte
A; Reference number: A90685; MUID:85225967
A; Accession: A90685
                         A;Title: Bovine alpha(1)-microglobulin/bikunin. Isolation and characterization of liv A;Reference number: $68149; MUID:96201710
A;Accession: $68149
A;Status: preliminary
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           homology; lipocali
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J. Biochem. 111, 681-687, 1992
A;Title: CDNA cloning and expression of rat tissue factor pathway inhibitor (TFPI).
A;Reference number: JX0213; MUID:92348361
A;Accession: JX0213
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  A; Molecule type: protein
A; Residues: 347-349 <HOC2>
R; Residues: 347-349 <HOC2>
R; Hochstrasser, K.; Albrecht, G.J.; Schonberger, O.L.; Wachter, E.
Hoppe-Seyler's Z. Physiol. Chem. 364, 1689-1696, 1983
A; Title: Kunitz-type proteinase inhibitors derived by limited proteolysis of A; Reference number: A91718; MUID:84133808
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            A; Molecule type: protein
A; Residues: 206-214, X', 216, X', 218-220 <CAS>
C; Superfamily: protein HC; animal Kunitz-type proteinase inhibitor homolog;
C; Superfamily: protein HC; animal Kunitz-type proteinase inhibitor homolog;
C; Keywords: duplication; glycoprotein; plasma; serine proteinase inhibitor
F; 35-188/Domain: lipocalin homology <LIP>
F; 231-281/Domain: animal Kunitz-type proteinase inhibitor homology <API>
F; 231-281/Domain: animal Kunitz-type proteinase inhibitor homology <API>
F; 241/Inhibitory site: Leu (chymotrypsin, elastase) #status experimental
F; 250/Binding site: carbohydrate (Asn) (covalent) #status experimental
F; 297/Inhibitory site: Arg (trypsin) #status experimental
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   229 DSCQLDYSQGPCLGLFKRYFYNGTSMACETFLYGGCMGNGNNFLSEKECLQTCRTV---- 284
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TGDLATSRNAADSSVPSAPRRQDSEDHSSDMFNYEEYCTANAVTGPCRASFPRWYFDVER 128
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ------EACNLPIVOGPCRSYIQLWAFDAVK 309
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             39;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         26.3%; Score 249.5; DB 1;
llarity 32.4%; Pred. No. 5.9e-15;
Conservative 16; Mismatches 45;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         A Contents: annotation; reactive sites
R;Gastillo, G.M.; Templeton, D.M.
FEBS Lett. 318, 292-296, 1993
A;Title: Subunit structure of bovine ESF (
A;Reference number: S31219; MUID:93178646
A;Accession: S31219
A;Status: preliminary
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          129 NSCNNFIYGGCRGNKNSYRSEEACMLRC 156
  98-106, 1996
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    tissue factor pathway inhibitor precursor
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Matches 48; Conserv
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A;Introns: 32/3; 104/2; 156/2; 207/1; 459/2; 536/3; 577/2; 1105/3; 1367/1; 1438/1; 1556/
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              - bovine
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  hypothetical protein C37C3.6b - Caenorhabditis elegans
C;Species: Caenorhabditis elegans
C;Date: 29-Oct-1999 #sequence_revision 29-Oct-1999 #text_change 01-Dec-2000
                                                                                                                                                                                                                                                         1265 OSMEDICRSRQDAGPCETYSDQWFYNAFSQECETFTYGGCGGNLNRFRSKDECEGRCFFV 1324
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          115
                                                                                                                                                                                                                                                                                                                              62 -----ATVTENATGDLATSRNAADSSVPSAPRRQDSEDHSSDMFNYEEYCTANAVTGPC 115
                                                                                                                                                                   Gaps
                                                                                                                                                                                                                    5 RSIHDFCLVSKVVGRCRASMPRWWYNVTDGSCQLFVYGGCDGNSNNYLTKEECLKKC--- 61
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    62 -----ATVTENATGDLATSRNAADSSVPSAPRRQDSEDHSSDMFNYEEYCTANAVTGPC
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                                                                                                       26.4%; Score 250.5; DB 2 30.1%; Pred. No. 2.3e-14; ive 26; Mismatches 79
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match 26.4%; Score 250.5; D
Best Local Similarity 30.1%; Pred. No. 3.2e-
Matches 49; Conservative 26; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      A; Gene: CESP: C37C3.6b; CESP: C37C3.6a
                                                                                                       Query Match 26.48
Best Local Similarity 30.18
Matches 49; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        C; Accession: T34395; T34394
                      A; Map position: '
C;Genetics:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              116
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A;Cross-references: EMBL:X54816; NID:g24475; PIDN:CAA38585.1; PID:g825614; EMBL:X5481 R;Diarra-Mehrpour, M.; Bourguignon, J.; Sesbouee, R.; Salier, J.P.; Leveillard, T.; M. Eur. J. Biochem. 191, 131-139, 1990
Bur. J. Biochem. 191, 131-139, 1990
A;Title: Structural analysis of the human inter-alpha-trypsin inhibitor light-chain g A;Reference number: S10778; MJID:90336621
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  A; Modecule type: mRNA
A; Residues: 1.352 «KAU>
A; Residues: 1.352 «KAU>
A; Cross-references: GB:X04494; NID:g24478; PIDN:CAA28182.1; PID:g24479
B; Copez Otin, C.; Grubb, A.O.; Mendez, E.
Arch. Biochem. Biophys. 228, 544-554, 1984
A; Title: The complete amino acid sequence of human complex-forming glycoprotein heter
A; Reference number: A90074; MUID:84126849
A; Accession: A90074
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A; Residues: 20-47;58-136,138-141,'T',143-144,146-198 <TAK>
A; Residues: 20-47;58-136,138-141,'T',143-144,146-198 <TAK>
A; Experimental source: pooled urine of patients with tubular proteinuria
B; Reisinger, P.; Hochstrasser, K.; Albrecht, G.J.; Lempart, K.; Saller, J.P.
Biol. Chem. Hoppe-Seyler 366, 479-483, 1985
A; Title: Human inter-alpha-trypsin inhibitor: localization of the kunitz-type domains
A; Reference number: A90686; MUID:85225968
A; Accession: A90686
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              A;Residues: 1-202 <DIA>
R;Raumeyer, J.F.; Polazzi, J.O.; Kotick, M.P.
Rikaumeyer, J.F.; Polazzi, J.O.; Kotick, M.P.
Nucleic Acids Res. 14, 7839-7850, 1986
A;Title: The mRNA for a proteinase inhibitor related to the HI-30 domain of inter-alp A;Reference number: A93642; MUID:87040757
A;Accession: A93642
                                                                                                                                               charge (HC)
                                                                                                                                                                                  rich protein
N;Contains: alpha-1-microglobulin (protein HC); inter-alpha-trypsin inhibitor
C;Species: Homo sapiens (man)
C;Date: 15-Oct-1982 #sequence_revision 30-Jun-1987 #text_change 08-Dec-2000
C;Accession: S13433; S10778; A93642; A90074; A90225; A90686; PN0450; B39079; A61580;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   persistent
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A; Molecule type: protein
A; Residues: 206-290, VI', 293-342, E', 344-350 <REI>
R; Atmani, F.; Lacour, B.; Strecker, G.; Parvy, P.; Drueeke, T.; Daudon, M.
Blochem. Blochem. Blochys. Res. Commun. 191, 1158-1165, 1993
A; Title: Molecular characteristics of uronic-acid-rich protein, a strong inhibitor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      s:
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A; Residues: 20-56,58-202 < LOP>
A; Residues: 20-56,58-202 < LOP>
A; Residues: 20-56,58-202 < LOP>
A; Residues: 20-56,58-202 < Lope  
A; Note: no evidence of sequence heterogeneity could be found, in spite of protein  
B; Takagi, T.; Takagi, K.; Kawai, T.
B; Takagi, T.; Takagi, K.; Kawai, T.
A; Title: Complete amino acid sequence of human alpha-1-microglobulin.
A; Reference number: A90225
A; Accession: A90225
                                                                                                        alpha-1-microglobulin/inter-alpha-trypsin inhibitor precursor [validated] N;Alternate names: bikunin; complex-forming glycoprotein heterogeneous in
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      I.B.; Rutherfurd,
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                                                                                                                                                                                                                                                                                                                                                                                                                                          R;Vetr, H.; Gebhard, W.
Biol. Chem. Hoppe-Seyler 371, 1185-1196, 1990
A;Title: Structure of the human alpha(1)-microglobulin-bikunin gene.
A;Réference number: S13433; MUID:91214554
A;Recession: S13433
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R; Enghild, J.J.; Salvesen, G.; Hefta, S.A.; Thogersen, J. Biol. Chem. 266, 747-751, 1991
A; Title: Chondroitin 4-sulfate covalently cross-links the A; Reference number: A39079; MUID:91093267
A; Recession: B39079
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A; Residues: 206-225 < ENG1>
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A;Molecule type: DNA
A;Residues: 1-352 <VET1>
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A; Molecule type: mRNA
A; Residues: 1:302 cRNJ>
A; Cross-references: DDBJ:D10926; NID:g220916; PIDN:BAA01724.1; PID:g220917
A; Experimental source: 11ver
C; Comment: This serine proteinase inhibitor regulates clotting by factor Xa-dependent in C; Comment: This serine proteinase inhibitor; animal Xunitz-type proteinase inhibitor
C; Comment: The first Kunitz-type domain binds the factor VIIa/tissue factor complex; the C; Comment: The first Kunitz-type domain binding the C; Superfamily: tissue factor pathway inhibitor; animal Xunitz-type proteinase inhibitor
C; Keywords: anticoagulant; blood coagulation; duplication; dlycoprotein; heparin binding F; 12-34 Domain: signal sequence *status predicted <SIG>F; 12-34 Domain: animal Xunitz-type proteinase inhibitor homology <BP>F; 12-103 Domain: animal Xunitz-type proteinase inhibitor homology <BP>F; 12-27 Domain: animal Xunitz-type proteinase inhibitor homology <BP>F; 28-29 Domain: animal Xunitz-type proteinase inhibitor homology <BP>F; 38-29 Domain: animal Xunitz-type proteinase inhibitor homology <BP>F; 28-29 Domain: animal Xunitz-type proteinase inhibitor homology <BP>F; 28-2
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C;Species: Ovis orientalis aries, Ovis ammon aries (domestic sheep)
C;Species: Ovis orientalis aries, Ovis ammon aries (domestic sheep)
C;Date: 31-Dec-1988 #sequence_revision 31-Dec-1988 #text_change 16-Jul-1999
C;Accession: A20652
B;Rasp, G; Hochstrasser, K; Wachter, E.; Reisinger, P.W.M.
Biol. Chem. Hoppe-Seyler 368, 727-731, 1987
A;Title: The amino-acid sequence of the trypsin-released inhibitor from sheep inter-alph A;Reference number: A20652; MUID:87299012
A;Reference number: A20652
A;Molecule type: protein
A;Residues: 1-123 cRAS
C;Superfamily: protein HC; animal Kunitz-type proteinase inhibitor homology; lipocalin P;F;S-SyDomain: animal Kunitz-type proteinase inhibitor homology <BP2>
F;61-111/Domain: animal Kunitz-type proteinase inhibitor homology <BP2>
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-----WCLEPADSGLCKA 233
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llarity 31.8%; Pred. No. 5.5e-15;
Conservative 15; Mismatches 47
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A; Molecule type: protein
A; Residues: 20-24 <CAL2>
R; Bourguignon, J.; Diarra-Mehrpour, M.; Sesboue, R.; Frain, M.; Sala-Trepat, J.M.; Ma Biochem. Biophys. Res. Commun. 131, 1146-1153, 1985
A; Title: Human inter-alpha-trypsin-inhibitor: characterization and partial nucleotide A; Reference number: 152208; MUID:86025577
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 A; Molecule type: protein
A; Residues: 89-100 (AKE>
R; Jessen, T.E.; Ploug, M.
R; Jessen, T.E.; Parang, K.L.; Ploug, M.
A; Title: Carbohydrate as covalent crosslink in human inter-alpha-trypsin inhibitor: a
A; Reference number: S02431; MUID:88167187
                                                                                                                                                                                                                                                                                                                                                                                                      R;Wojcik, E.G.C.; van den Berg, M.; van der Linden, I.K.; Poort, S.R.; Cupers, R.; Be Blochem. J. 311, 753-759, 1995
A;Title: Factor IX Zutphen: a Cys(18) -> Arg mutation results in formation of a heter A;Reference number: S59509; MUID:96067589
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        A;Molecule type: protein
A;Residues: 27-35, Y', 37 <MOJ>
A;Residues: 27-35, Y', 37 <MOJ>
E. A;Amani, F.; Mizon, J.; Khan, S.R.
Eur. J. Biochem. 236, 984-990, 1996
A;Title: Identification of uronic-acid-rich protein as urinary bikunin, the light cha A;Reference number: $66434; MUID:96270753
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A; Contents: annotation; variant of alpha-1-microglobulin
A; Contents: annotation; variant of alpha-1-microglobulin
A; Note: pooled urine samples contained two forms of this protein, both lacking 57-Lys
B; Hochstrasser, K.; Schonberger, O.L.; Rossanith, I.; Wachter, E.
Hoppe-Seyler's Z. Physiol. Chem. 362, 1357-1362, 1981
A; Title: Kunitz-type proteinase inhibitors derived by limited proteolysis of the inte
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A. Residues: 206-214, X', 216-230 (ATM2)
A. Residues: 206-214, X', 216-230 (ATM2)
R. Akerstroem, B.; Bratt, T.; Enghild, J.J.
FEBS Lett. 362, 50-54, 1995
A. Title: Formation of the alpha(1)-microglobulin chromophore in mammalian and insect
A. Reference number: S68728; MUID:95212582
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A;Residues: 206-214, X',216-217 <JES>
K:Lopez, C.; Grubb, A.; Mendez, E.
FEBS Lett. 144, 349-353, 1982
A;Title: Human protein HC displays variability in its carboxyl-terminal amino acid
                                                                                                                                                                                                                   A.Accession: 152208
A.Stettus: translated from GB/EMBL/DDBJ
A.Molecule type: mRNA
A.Residues: 302-352 <BOUD>
A.Cross-references: GB:M11562; NID:g186587; PIDN:AAA59194.1; PID:g307077
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   DFCLVSKVVGRCRASMPRWWYNVTDGSCQLFVYGGCDGNSNNYLTKEECLKKCATVTENA 68
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             by affinity chromatography.
A.Reference number: A91688; MUID:82074265
A.Contents: annotation; carbohydrate binding sites
R.Morii, M.; Travis, J.
Biol. Chem. Hoppe-Seyler 366, 19-21, 1985
A.Title: The reactive site of human inter-alpha-trypsin inhibitor is A; Reference number: A90602; MUID:85225940
A; Reference number: A90602; MUID:85225940
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Length 352;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match
Best Local Similarity
Matches 48; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               A; Accession: S59509
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         A; Accession: S68728
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          A; Accession: S02431
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   6
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FIGURES, T. B. Balduck, M. J. Standard, C.: Laroul, S.: Sutier, P.; Mizon, J. Tit., I glochem 237 2711;2371;2371;2371; Single C.: Balduck, M. Standard, M. Standa
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Alternate names: bikunin; ITI: PI-14 (inhibitor precursor - pig (fragment)
N.Alternate names: bikunin; ITI: PI-14 (inhibitory fragment of ITI)
C.Species: Sus scrofa domestica (domestic pig)
C.Spate: 30-Unn-1987 #sequence_revision 04-Feb-2000 #text_change 04-Feb-2000
C.Satession: S11066; S13493; A01208
R.Gebhard, W.; Schreitmueller, T.; Vetr, H.; Wachter, E.; Hochstrasser, K.
FBBS Lett. 269, 32-36, 1990
A.Title: Complementary DNA and deduced amino acid sequences of porcine alphal-migrogl A.Reference number: S11066; MUID:90353595
A.Status: preliminary
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     A Molecule type: protein A. Molecule type: protein A. Molecule type: protein A. Molecule type: protein A. Residues: 212-258, 'O', 260-269, 'S', 271-277, 'O', 279-282, 'A', 284, 'IR', 287-292, 'A', 294-C; Comment: This inhibitory fragment, released from native ITI after limited proteolys first domain interacts weakly with PMN-granulocytic elastase and not at all with pane C; Comment: The amino acid at position P2' (228-Met) appears to determine the specific
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    A;Cross-references: EMBL:X53685; NID:91877; PIDN:CAA37725.1; PID:91878
R;Tavakkol, A.
Biochim. Biophys. Acta 1088, 47-56, 1991
A;Title: Molecular cloning of porcine alpha(1)-microglobulin/HI-30 reveals developmen A;Reference number: S13493; MUID:91113729
A;Accession: S13493
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               predicted
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C:Superfamily: protein HC; animal Kunitz-type proteinase inhibitor homology C:Superfamily: protein HC; animal Kunitz-type proteinase inhibitor homology.
C:Superfamily: protein HC; animal Kunitz-type proteinase inhibitor proteinase inhibitor.
E:20-236/Domain: animal Kunitz-type proteinase inhibitor homology <BP1>
E:216-266/Domain: animal Kunitz-type proteinase inhibitor homology <BP2>
E:216-266/Domain: animal Kunitz-type proteinase inhibitor homology <BP2>
E:226-227-249,241-262,272-322,281-305,297-318/Poisulfide bonds: #status F:226/Inhibitory site: Leu (chymotrypsin, elastase) #status predicted
E:235/Binding site: carbohydrate (Asn) (covalent) #status experimental
E:282/Inhibitory site: Arg (trypsin) #status predicted
                                                                                                                                               :: | || : | || : || :| :| :| || 43 QKPTHSFCAMKVDDGPCRAYIKRFFNILAHQCEEFIYGGCEGNENRFESLEECKEKCAR 102
                                                                                                                                                                                                                                          VTENATGDLATSRNAADSSVPSAPRRQDSEDHSSDMFNYEEYCTANAVTGPCRASFPRWY 123
                                                                                                                                                                                                                                                                                                         --FCFLEEDPGICRGYITRYF 138
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Gaps
                                                                                                     4 ERSIHDFCLVSKVVGRCRASMPRWWYNVTDGSCQLFVYGGCDGNSNNYLTKEECLKKCAT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  9 DFCLVSKVVGRCRASMPRWWYNVTDGSCQLFVYGGCDGNSNNYLTKEECLKKCATVTENA
                                      28;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      39;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Indels
                                          Indels
1.9e-14;
ches 61;
                                                                                                                                                                                                                                                                                                                                                                            124 FDVERNSCNNFIYGGCRGNKNSYRSEEACMLRCFRQQENP 163
                                                                                                                                                                                                                                                                                                                                                                                                               Score 242.5; DB 1;
Pred. No. 2.4e-14;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      43;
       Pred. No. 1.96
; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Mismatches
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                                      23;
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       30.08;
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Best Local Similarity 31.8
Matches 47; Conservative
   Similarity 30.0
18; Conservative
                                                                                                                                                                                                                                                                                                         DYPKMTTKLTFOKGKPD-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         A; Molecule type: mRNA
A; Residues: 1-337 <GEB>
       Best Local
                                      Matches
                                                                                                                                                                                                                                                                                                         103
                                                                                                                                                                 Db
                                                                                                                                                                                                                                                                                                         g
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Nilternate names: endothelial cell coagulation inhibitor; endothelial cell tissue facto
Cispecies: Oryctolagus cuniculus (domestic rabbit)
Rydcession: S12143; A61373
Rydcession: S12143; MuID: 91057146
A; Reference number: S12143; MuID: 91057146
A; Reference number: S12143; MuID: 91057146
A; Residues: 1:300 cwES
A; Cross-references: EMBL:X54708; NID: 91612; PIDN: CAA38515.1; PID: 91613
A; Residues: 1:300 cwES
A; Cross-references: EMBL:X54708; NID: 9194927
A; Reference number: A61373; MuID: 91349227
A; Recession: A61373
A; Molecule type: protein
A; Residues: 25-33, Xx, 35-46 cCOL>
C; Superfamily: tissue factor pathway inhibitor; animal Kunitz-type proteinase inhibitor homology cBP1>
C; Superfamily: tissue factor pathway inhibitor homology cBP1>
C; Superfamily: tissue factor pathway inhibitor homology cBP1>
C; Superfamils: animal Kunitz-type proteinase inhibitor homology cBP3>
F; 213-171/Domain: animal Kunitz-type proteinase inhibitor homology cBP3>
F; 213-263/Domain: animal Kunitz-type proteinase inhibitor homology cBP3>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             A; Cross-references: CB:S61902; NID:g386015; PIDN:AAB26836.1; PID:g386016
C; Superfamily: tissue factor pathway inhibitor: animal Kunitz-type proteinase inhibitor
E; 49-99/Domain: animal Kunitz-type proteinase inhibitor homology <BPII:
F; 120-170/Domain: animal Kunitz-type proteinase inhibitor homology <BPII>
F; 212-262/Domain: animal Kunitz-type proteinase inhibitor homology <BPI>
F; 212-262/Domain: animal Kunitz-type proteinase inhibitor homology <BPII>
                                                                                                                                                                                                                                                                                           C;Species: Oryctolagus cuniculus (domestic rabbit)
C;Date: 04-Sep-1997 #sequence_revision 04-Sep-1997 #text_change 13-Aug-1999
C;Date: 04-Sep-1997 #sequence_revision 04-Sep-1997 #text_change 13-Aug-1999
C;Accession: 146937
R;Belaaouaj, A.; Kuppuswamy, M.N.; Birktoft, J.J.; Bajaj, S.P.
Thromb. Res. 69, 547-553, 1993
A;Title: Revised cDNA sequence of rabbit tissue factor pathway inhibitor.
A;Accession: 146937
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Mesduce: 1-299 <BEL>
A;Residues: 1-299 <BEL>
A;Residues: 1-299 <BEL>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        64 VTENATGDLATSRNAADSSVPSAPRRQDSEDHSSDMFNYEEYCTANAVTGPCRASFPRWY 123
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           --FCFLEEDPGICRGYITRYF 137
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 4 ERSIHDFCLVSKVVGRCRASMPRWWYNVTDGSCQLFVYGGCDGNSNNYLTKEECLKKCAT 63
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      28;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Length 299;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Length 300;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  61; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        FDVERNSCNNFIYGGCRGNKNSYRSEEACMLRCFRQQENP 163
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            25.7%; Score 244; DB 2; 30.0%; Pred. No. 1.5e-14; ive 23; Mismatches 61.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      DB 2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      25.6%; Score 243;
                                                                  310 GKCVLFPYGGCQGNGNKFYSEKECREYC 337
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match
Best Local Similarity 30.0%;
Matches 48; Conservative
                                                                                                                                                                                                                                                                   tissue factor pathway inhibitor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      DYPKMTTKLTFQKGKPD-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match
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A, Title: Rat alpha(1) - microglobulin: co-expression in liver with the light chain of i
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                                                                                                                                                                                                                                                  A;Introns: 33/1; 56/1; 100/1; 142/3; 271/3; 451/1; 525/3; 774/1; 1093/1; 1178/1; 1221
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                                                                                                                                                                                                                                                                                                                                                                                                        ;;
A;Molecule type: DNA
A;Residues: 1-2225 <WIL>
A;Cross-references: EMBL:292815; PIDN:CAB07294.1; GSPDB:GN00023; CESP:W01F3.3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             alpha-1-microglobulin/inter-alpha-trypsin inhibitor light chain precursor NyAlternate names: acid-stable proteinase inhibitor; bikunin; trypstatin C;Species: Rattus norvegicus (Norway rat) C;Cpecies: Rattus norvegicus (Norway rat) C;Date: 22-Nov-1993 #sequence_revision 01-Sep-1995 #text_change 04-Feb-2000 C;Accession: $21089, A53056, A22995; A31890; A61633 RS:Lindqvist, A.; Bratt, T.; A11810, A31810; A3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   tissue factor pathway inhibitor - rabbit
C;Species: Oryctolagus cuniculus (domestic rabbit)
C;Date: 01-Aug-1995 #sequence_revision 01-Sep-1995 #text_change 16-Jul-1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TGDLATSRNAADSSVPSAPRRQDSEDHSSDMFNYEEYCTANAVTGPCRASFPRWYFDVER 128
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         65 TENATGDLATSRNAADSSVPSAPRRQDSEDHSSDMFNYEEYCTANAVTGPCRASFPRWYF 124
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          11 CLVSKVVGRCRASMPRWWYNVTDGSCQLFVYGGCDGNSNNYLTKEECLKKC--ATVTENA
                                                                                                                                                                                                                                                                                                                                                                                                        32;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  23;
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                                                                                                                                                                                                                                                                                                                              Length 2225;
                                                                                                                                                                                                                                                                                                                                                                                                        Indels
                                                                                                                                                                                                                                                                                                                              25.3%; Score 240; DB 2; 29.3%; Pred. No. 2.9e-13;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         129 NSCNNFIYGGCRGNKNSYRSEEACMLRCFRQQENPPL 165
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               867 QDCRAFTYGGGGGNGNNFATMQECRSRCVMAMKKSPV 903
                                                                                                                                                                                                                                                                                                                                                                                                        21; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     DVERNSCNNFIYGGCRGNKNSYRSEEACMLRC 156
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Rigirard, T.J.; Gallani, D.; Broze Jr., G.J. Biochem. J. 303, 923-928, 1994
A/Title: Complementary DNA sequencing of can A;Reference number: S53325; MUID:95071310
A;Accession: S53325
                                                                                                       A:Experimental source: clone WOlF3 C;Genetics:
                                                                                                                                                                                                                                                                                                                                                                                                        Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     45; Conservative
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Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                             Best_Local Similarity
Matches 46; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          A; Status: preliminary
A; Molecule type: mRNA
A; Residues: 1-396 <GIR>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    837 TPD-----
                                                                                                                                                                                    A; Gene: CESP: W01F3.3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Accession: $53325
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  107 YPKA----
                                                                                                                                                                                                                           A; Map position:
                                                                                                                                                                                                                                                                                                                                      Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           125
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C;Species: Caenorhabditis elegans
C;Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 15-Oct-1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      69 TGDLATSRNAADSSVPSAPRRQDSEDHSSDMFNYEEYCTANAVTGPCRASFPRWYFDVER 128
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Gaps
   294
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ---CNLPIVQGPCRAFIRLWAFDAAQ 85
   EACSLPIVSGPCRGFFQLWAFDAVQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          39;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   47;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               submitted to the EMBL Data Library, March 1997
A; Reference number: 220145
A; Accession: T26063
A; Status: preliminary; translated from GB/EMBL/DDBJ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          25.5%; Score 241.5; DB 31.8%; Pred. No. 1e-14;
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                                                                         129 NSCNNFIYGGCRGNKNSYRSEEACMLRC 156
                                                                                                                          GRCVLFNYGGCOGNGNOFYSEKECKEYC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               47; Conservative
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Best Local Similarity
Matches 47; Conserv
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A; Molecule type: mRNA
A; Residues: 1-304 < KAMA
A; Cross-references: GB:S7337; NID:9685016; PIDN:AAB31955.1; PID:9685017
A; Experimental source: liver
C; Comment: This protein inhibits the activities of factor Xa and tissue factor factor
C; Comment: This protein inhibits the activities of factor xa and tissue factor factor
C; Superfamily: tissue factor pathway inhibitor; animal Kunitz-type proteinase inhibitor
E; 1-28 / Domain: signal sequence #status predicted < SIGs
F; 1-38 / Domain: animal Kunitz-type proteinase inhibitor homology < BP1-
F; 1-25 / Domain: animal Kunitz-type proteinase inhibitor homology < BP1-
F; 1-26 / Domain: animal Kunitz-type proteinase inhibitor homology < BP2-
F; 1-27 / 27 / Domain: animal Kunitz-type proteinase inhibitor homology < BP3-
F; 1-26 / Domain: animal Kunitz-type proteinase inhibitor homology < BP3-
F; 1-26 / Domain: animal Kunitz-type proteinase inhibitor complex) #status predicted
F; 135 / Inhibitory site: Lys (coagulation factor X) #status predicted
F; 145, 195, 266/Binding site: carbohydrate (Asn) (covalent) #status predicted
F; 127 / Inhibitory site: Arg (unidentified proteinase) #status predicted
D. Blochem. 115, 708-714, 1994
A; Title: Amino acid sequence and inhibitory activity of rhesus monkey tissue factor p A; Reference number: JC2264; MUID:94375417
A; Moleonal Amino acid sequence and inhibitory activity of rhesus monkey tissue factor p A; Reference number: JC2264; MUID:94375417
A; Moleonal Activity of A; Moleonal A
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            69 TG----DLATSRNAADSSVPSAPRRQDSEDHSSDMFNYEEYCTANAVTGPCRASFPRWYF 124
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               9 DFCLVSKVVGRCRASMPRWWYNVTDGSCQLFVYGGCDGNSNNYLJTKEECLKKCATVTENA 68
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      24.9%; Score 236.5; DB 1; Length 304; 34.9%; Pred. No. 7.4e-14; tive 24; Mismatches 64; Indels 11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 DVERNSCNNFIYGGCRGNKNSYRSEEACMLRC 156
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Best Local
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"Residues: 205-213, X', 215-229, N', 231-232, K', 234-238 <SUG>
"Residues: 205-213, X', 215-229, N', 231-232, K', 234-238 <SUG>
"Residues: 205-213, X', 215-229, N', 231-232, K', 234-238 <SUG>
"Residues: 205-213, X', 215-229, N', 231-232, K', 234-238 <SUG>
"Superfamily: protein HC: animal Kunitz-type proteinses inhibitor page in plasma; serin plasma: signal sequence #status predicted <SIG>
"20-20-20/Product: alpha-1-microglobulin #status predicted <Alm>
"34-187/Domain: lipocalin homology <LIP>
"205-349/Product: inter-alpha-trypsin inhibitor #status experimental <IAI>
"34-80/Domain: animal Kunitz-type proteinase inhibitor homology <BPD>
"24/Binding site: carbohydrate (7hr) (covalent) #status predicted
"55/Cross-1ink: alpha-1-microglobulin-ig alpha complex chromophore (Cys) (interchain to "55/Cross-1ink: alpha-1-microglobulin-ig alpha complex chromophore (Cys) (interchain to "514/Binding site: chondroitin sulfate (Ser) (covalent) #status experimental
"226/Inhibitory site: Arg (trypsin) #status predicted
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   tissue factor pathway inhibitor precursor - rhesus macaque
N'Alternate names: extrinsic pathway inhibitor; lipoprotein-associated coagulation inhib
S'Species: Macaca mulatta (rhesus macaque)
C'Date: 10-Sep-1999 #sequence_revision 10-Sep-1999 #text_change 21-Jul-2000
C'Accession: JC2264
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     A;Accession: A25935
A;Molecule type: protein
A;Residues: 141, A',143-195
R;Kido, H.; Yokogoshi, Y.; Katunuma, N.
B;Sido, H.; Yokogoshi, Y.; Katunuma, N.
A; Biol. Chem. 253, 18104-18107, 1988
A;Title: Kunitz-type protease inhibitor found in rat mast cells. Purification, propertie
A;Reference number: A31890; MUID:89053978
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R;Itch, H.; Ide, H.; Ishikawa, N.; Nawa, Y.
J. Biol. Chem. 269, 3818-3822, 1994
A;Title: Mast cell protease inhibitor, trypstatin, is a fragment of inter-alpha-trypsin A;Reference number: A53056; MUID:94148892
A;Accession: A53056
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A; Residues: 283-301, L',303-322, N',324-329, PK',332-333, W',335-343 <KID>
R; Sugiki, M; Maruyama, M; Yoshida, E.; Sumi, H.; Mihara, H.
Inflammation 15, 281-289, 1991
A; Title: Acid-stable protease inhibitor in chronic phase of carrageenin-induced inflamma
A; Reference number: A61633; MUID:92120777
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A;Residues: 285-341 <ITO>
R;Resitues: 285-341 <ITO>
R;Kastern, W: Bjorck, L.; Akerstrom, B.
Biol. Chem. 261, 15070-15074, 1986
A;Title: Developmental and tissue-specific expression of alpha-1-microglobulin mRNA in A;Reference number: A25935; MUID:87033744
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SUMMARIES

Result No.

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Marlor CW, Muller DK, Tamburini PP;

Davis G, Delaria KA, WPI; 1997-470876/43.

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standard; P	Protein;	170 AA.		
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MayOU41;  )-APR-1998 (first entry liman placental bikunin.  aman; placental bikunin;  asmin; factor XIIa; traiting probaemia; perioperative cood coagulation disease stric cancer; cervical.  mo sapiens.  )-XEP-1997; 97WO-US038  1-OCT-1996; 96US-00131  THAR-1997; 96US-00131  THAR-1997; 96US-00131	bikunin.  bikunin.  l bikunin; in XIII - treatin fection; gra pperalive blo on disease; p ocrvical can orvical can 97WO-US03894.	hith ent nul od oly cer	ition; trypsin; ke ;; prevention; oed omatosis; multiple loss; sepsis; sho trauma; stroke; he ;; metastasis; bloc	Adward 1998 (first entry)  20-APR-1998 (first entry)  Human placental bikunin.  Human; placental bikunin; inhibition; trypsin; kallikrein;  plasmin; factor XIIa; treatment; prevention; oedema;  linflammation; infection; granulomatosis; multiple sclerosis;  ischaemia; perioperative blood loss; sepsis; shock; fibrosis;  blood coagulation disease; polytrauma; stroke, haemorrhage;  gastric cancer; cervical cancer; metastasis; blood loss.  Homo sapiens.  W09733996-A2.  18-SEP-1997;  97WO-US03894.  10-MAR-1996; 96US-0013106.

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                                                                                                                     The present sequence is a human placental bikunin, which inhibits, e.g. trypsin, kallikrein, plasmin and factor XIIa. Bikunin can be used to treat or prevent brain and spinal cord oedeme, inflammation, infection or granulomatosis, multiple sclerosis, ischaemia, perioperative blood loss, sepsis, shock, fibrosis, blood coagulation diseases, polytrauma, stroke, cerebral or subarachhoid hemorrhage and gastric or cervical cancer and prevent metastasis. It is particularly useful for reducing blood loss during surgery, and can also be used to treat other cancer, arthritis, anaemia, non-insulin dependent diabetes, influenza and similar viral infections, acute pancreatitis and gout, and prevent pre-term labour. It has similar properties to aprotinin, but is less highly charged so should be less immunogenic and less likely to damage the Kidneys. Manipulation of the bikunin sequence may allow the inhibitory profile to be altered. It also reduces or eliminates the need for whole donor blood or blood products during surgery, thereby reducing the risk of infection and other adverse side effects, as well as reducing
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       New human placental bikunin - used to inhibit kallikrein, trypsin etc. in treatment of oedema, multiple sclerosis, fibrosis, or
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Length 170;
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100.0%; Pred. No. 4e-89;
Live 0; Mismatches 0;
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                                                                                         Claim 1; Page 65; 110pp; English.
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                                                     perioperative blood loss
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(FARB ) BAYER

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Mucociliary dysfunction is the inability of ciliated epithelium to clear mucus and sputum in lung airways. Mucociliary dysfunction is a serious complication of chronic obstructive lung diseases such as Chronic Costruction of chronic obstructive lung diseases such as Chronic costructions (CE).

In addition, patients suffering from mucociliary dysfunction are susceptible to secondary bacterial infections. The present sequence is a sequence for human placental bixunin protein. This sequence was derived from a human placental bixunin protein. This sequence was derived from a human placental cDNA library by PCR-based amplification. This protein is a Kunitz-type serine protease inhibitor protein, which can stimulate the rate of mucociliary clearance of mucus and sputum in lung airways. Therefore, the present protein may be used for treating lung diseases such as CF, CB, BE, and chronic sluusitis and glue ear which are caused by retention and accumulation of mucus.

Note: the present sequence is defined as SEQ ID 51 in the sequence is clearly shown as a nucleotide sequence. Therefore, the nucleotide cleary shown as a nucleotide sequence. Therefore, the nucleotide cleary shown as a nucleotide sequence.
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                                                                                         Stimulating mucociliary clearance rate of mucus and sputum in lung airways for treating lung diseases such as cystic fibrosis and bronchitis involves administering a Kunitz-type serine protease inhibitor -
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   100.0%; Score 948; DB 21; Length 170; 100.0%; Pred. No. 4e-89; ive 0; Mismatches 0; Indels 0
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                  Taylor WJA;
                                                                                                                                                                                              Disclosure; Pages 166-167; 173pp; English.
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                  Newton BB,
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Matches 170; Conservative
                  Poll CT,
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trypsin

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Human; mucociliary dysfunction; mucus; sputum;
chronic obstructive lung disease; chronic bronchitis; CB; Bronchiectasis;
BE; asthma; cystic fibrosis; CF; bacterial infection; placental bikunin;
Kunltz-type serine protease inhibitor; chronic sinusitis; glue ear.
                                                                                                                                                                                                                                                                                                                                                          The present sequence is a human placental bikunin, which inhibits, e.g. trypsin, kallikrein, plasmin and factor XIIa. Bikunin can be used to treat or prevent brain and spinal cord coedema, inflammation, infection or granulomatosis, multiple sclerosis, ischaemia, perioperative blood loss, sepsis, shock, fibrosis, blood coagulation diseases, polytrauma, stroke, crebral or subarachnoid hemorrhage and gastric or cervical cancer and prevent metastasis. It is particularly useful for reducing blood loss during surgery, and can also be used to treat other cancer, arthritis, anemia, non-insulin dependent diabetes, influenza and similar viral infections, acute pancreatitis and oprotinin, but is less highly charged so should be less immunogenic and less likely to damage the kidneys. Manipulation of the bikunin sequence may allow the inhibitory profile to be altered. It also reduces or eliminates the need for whole donor blood or blood betting squence side effects, as well as reducing
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sclerosis, fibrosis, or
                                                                                                                                         Tamburini PP;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     121 RWYFDVERNSCNNFIYGGCRGNKNSYRSEEACMLRCFRQQENPPLPLGSK 170
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        100.0%; Score 948; DB 18;
100.0%; Pred. No. 4.2e-89;
ive 0; Mismatches 0;
                                                                                                                                       Muller DK,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Mature human placental bikunin protein.
                                                                                                                                                                                                                            human placental bikunin - used to . in treatment of oedema, multiple
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               AAB14159 standard; protein; 179 AA.
                                                                                                                                       Marlor CW,
                                                                                                                                                                                                                                                                                                                       Claim 1; Page 67; 110pp; English.
96US-0725251.
96US-0013106.
96US-0019793.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Matches 170; Conservative
                                                                                                                                                                                                                                                                              perioperative blood loss
                                                                                                                                       Davis G, Delaria KA,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                the cost of surgery.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Best Local Similarity
                                                                                                                                                                                  WPI; 1997-470876/43.
                                                                                            (FARB ) BAYER CORP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              WO200037099-A2
04-OCT-1996;
11-MAR-1996;
14-JUN-1996;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              AAB14159;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  AAB14159
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ò
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                                                                                                                                                                                                                                                                                                                                Mucociliary dysfunction is the inability of ciliated epithelium to clear mucus and sputum in lung airways. Mucociliary dysfunction is a serious complication of chronic obstructive lung diseases such as chronic benchiectasis (BE), asthma and Cystic Fibrosis (CF). In addition, patients suffering from mucociliary dysfunction are susceptible to secondary bacterial infections. The present sequence is a sequence for human placental bikunin protein. This sequence is protein is a Kunitz-type serine protease inhibitor protein, which can stimulate the rate of mucociliary diearance of mucus and sputum in lung aliways. Therefore, the present protein may be used for treating lung diseases such as CF, CB, BE, and chronic sinusitis and glue ear which are caused by retention and accumulation of mucus.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1 ADRERSIHDFCLVSKVVGRCRASMPRWWYNVTDGSCQLFVYGGCDGNSNNYLTKEECLKK 60
                                                                                                                                                                          Stimulating mucociliary clearance rate of mucus and sputum in lung airways for treating lung diseases such as cystic fibrosis and bronchitis involves administering a Kunitz-type serine protease
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match 100.0%; Score 948; DB 21; Length 170; Best Local Similarity 100.0%; Pred. No. 4e-89; Matches 170; Conservative 0; Mismatches 0; Indels 0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Human; placental bikunin; inhibition; trypsin; kallikrein; plasmin; factor XIIa; treatment; prevention; oedema; inflammation; infection; granulomatosis; multiple sclerosis; ischaemia; perioperative blood loss; sepsis; shock; fibrosis; blood coagulation disease; polytrauma; stroke; haemorrhage; gastric cancer; cervical cancer; metastasis; blood loss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Taylor WJA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                AAW30053 standard; Protein; 179 AA.
                                                                                                                                                                                                                                                                                               Claim 14; Page 90; 173pp; English.
                                                                                       Newton BB,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    97WO-US03894
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Human placental bikunin.
                                                                                                                                  WPI; 2000-452127/39.
                                                                                     Poll CT,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              170 AA;
                                        (FARB ) BAYER
17-NOV-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         W09733996-A2
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Homo sapiens
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                                                                                                                                                                                                                                                  inhibitor
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence
                                                                                     Hall R,
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AAW30053 RESULT

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Human; mucociliary dysfunction; mucus; sputum;
chronic obstructive lung disease; chronic bronchitis; CB; Bronchiectasis;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 61 CATVTENATGDLATSRNAADSSVPSAPRRQDSEDHSSDMFNYEEYCTANAVTGPCRASFP 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           19 ADRERSIHDFCLVSKVVGRCRASMPRWWYNVTDGSCQLEVYGGCDGNSNNYLTKEECLKK 78
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1 ADRERSIHDFCLVSKVVGRCRASMPRWWYNVTDGSCQLFVYGGCDGNSNNYLTKEECLKK
                                                                                                                                                                                                                                                                                                                                                                   New human placental bikunin - used to inhibit kallikrein, trypsin etc. in treatment of oedema, multiple sclerosis, fibrosis, or
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Length 197;
                                                                                                                                                                                                                                                                            Tamburini PP;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           139 RWYFDVERNSCNNFIYGGCRGNKNSYRSEEACMLRCFRQOENPPLPLGSK 188
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 121 RWYFDVERNSCNNFIYGGCRGNKNSYRSEEACMLRCFRQQENPPLPLGSK 170
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Human placental bikunin mature protein and signal peptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Score 948; DB 18;
Pred. No. 4.8e-89;
Mismatches 0;
                                                                                                                                                                                                                                                                            Muller DK,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ΑĄ
                                                                                                                                                                                                                                                                            Marlor CW,
                                                                                                                                                                                                                                                                                                                                                                                                                                                           Claim 1; Page 65; 110pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       100.0%; Sc
100.0%; Pr
tive 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           AAB14160 standard; protein; 197
                                                                                                                                    96US-0725251.
96US-0013106.
96US-0019793.
                                                                                          97WO-US03894
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                                                                                                                                                                                                                                                                                                                                                                                                                perioperative blood loss
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Best Local Similarity 100.
Matches 170; Conservative
                                                                                                                                                                                                                                                                            Delaria KA,
                                                                                                                                                                                                                                                                                                                         WPI; 1997-470876/43.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       the cost of surgery
                                                                                                                                                                                                                                 (FARB ) BAYER CORP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            197 AA;
W09733996-A2
                                                                                          10-MAR-1997;
                                                                                                                                                            11-MAR-1996;
14-JUN-1996;
                                             18-SEP-1997
                                                                                                                                       04-0CT-1996;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence
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                                                                                                                                                                                                                                                                            Davis G,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              RESULT 7
AAB14160
ID AAB1
    g
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Mucocillary dysfunction is the inability of ciliated epithelium to clear mucus and sputum in lung airways. Mucocillary dysfunction is a serious complication of chronic obstructive lung diseases such as Chronic Exponential (CB), Bronchiectasis (BE), asthma and Cystic Fibrosis (CF). In addition, patients suffering from mucocillary dysfunction are susceptible to secondary bacterial infections. The present sequence is human placental bikunin. This protein is a Kunitz-type serine protease inhibitor protein, which can stimulate the rate of mucocillary clearance of mucus and sputum in lung airways. Therefore, the present protein may be used for treating lung diseases such as CF, CB, BE, and chronic sinusitis and glue ear which are caused by retention and accumulation of mucus. The present sequence is the mature human placental bikunin protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       61 CATVTENATGDLATSRNAADSSVPSAPRRQDSEDHSSDMFNYEEYCTANAVTGPCRASFP 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CATVIENATGDLATSRNAADSSVPSAPRRQDSEDHSSDMFNYEEYCTANAVTGPCRASFP 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Gaps
                                                                                                                                                                                                                                                                                                                      d sputum in lung fibrosis and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1 ADRERSIHDFCLVSKVVGRCRASMPRWWYNVTDGSCQLFVYGGCDGNSNNYLTKEECLKK
                                                                                                                                                                                                                                                                                                                    Stimulating mucociliary clearance rate of mucus and sputum in luairways for treating lung diseases such as cystic fibrosis and bronchitis involves administering a Kunitz-type serine protease
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Length 179;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      plasmin; factor XIIa; treatment; prevention; oedema; inflammation; infection; granulomatosis; multiple sclerosis; ischaemia; perioperative blood loss; sepsis; shock; fibrosis; blood coagulation disease; polytrauma; stroke; haemorrhage; gastric cancer; cervical cancer; metastasis; blood loss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    121 RWYFDVERNSCNNFIYGGCRGNKNSYRSEEACMLRCFRQQENPPLPLGSK 170
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Human; placental bikunin; inhibition; trypsin; kallikrein;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Score 948; DB 21;
Pred. No. 4.2e-89;
Mismatches 0;
                                                                                                                                                                                                                              Taylor WJA;
                                                                                                                                                                                                                                                                                                                                                                                                                                   Claim 14; Pages 89-90; 173pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 AAW30043 standard; Protein; 197 AA
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                                                                                                                                                                                                                            Poll CT, Newton BB,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Ouery Match 100.0%;
Best Local Similarity 100.0%;
Matches 170; Conservative 0
                                                                                                             98US-0218913
99US-0441966
                                                                  99WO-GB04381
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      20-APR-1998 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Human placental bikunin.
                                                                                                                                                                                                                                                                         WPI; 2000-452127/39.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  179 AA;
                                                                                                                                                                                 (FARB ) BAYER AG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Homo sapiens
                                                                                                          22-DEC-1998;
17-NOV-1999;
                                                                22-DEC-1999;
                     29-JUN-2000
                                                                                                                                                                                                                                                                                                                                                                                      inhibitor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        sednence
                                                                                                                                                                                                                            Hall R,
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AAW30043

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Gaps

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us-09-218-913d-52.rag

placental bikunin; inhibition;

Human placental bikunin.

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BE; asthma; cystic fibrosis; CF; bacterial infection; placental bikunin; Kunitz-type serine protease inhibitor; chronic sinusitis; glue ear.
                                                                                                                                                                                                                  Stimulating mucociliary clearance rate of mucus and sputum in lung airways for treating lung diseases such as cystic fibrosis and bronchitis involves administering a Kunitz-type serine protease
                                                                                                                                                                                   Taylor WJA;
                                               1..18
/label= Signal_peptide
19..197
/label= Mature_protein
                                        Location/Qualifiers
                                                                                                                                                                                   Poll CT, Newton BB,
                                                                                                                          99WO-GB04381
                                                                                                                                         98US-0218913
99US-0441966
                                                                                                                                                                                                  WPI; 2000-452127/39.
                                                                                                                                                                  (FARB ) BAYER AG.
                                                                                        WO200037099-A2
                        Homo sapiens
                                                                                                                                         22-DEC-1998;
17-NOV-1999;
                                                                                                         29-JUN-2000
                                                                                                                                                                                                                                           inhibitor
                                                                                                                                                                                  Ж,
                                                Peptide
                                                                 Protein
                                                                                                                                                                                  Hall
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Mucociliary dysfunction is the inability of ciliated epithelium to clear mucus and sputum in lung airways. Mucociliary dysfunction is a serious complication of chronic obstructive lung diseases such as Chronic Eronchitis (CB), Bronchiectasis (BE), asthma and Cystic Fibrosis (FF). In addition, patients suffering from mucociliary dysfunction are musceptible to secondary bacterial infections. The present sequence is human placental bikunin. This protein is a Kunitz-type serine protease inhibitor protein, which can stimulate the rate of mucociliary clearance of mucus and sputum in lung airways. Therefore, the present protein may be used for treating lung diseases such as CF, CB, BE, and chronic sinusitis and glue ear which are caused by retention and accumulation of mucus. The present sequence is the full-length human placental bikunin Claim 13; Page 88; 173pp; English. protein sequence,

197 AA; Sequence

Gaps Length 197; 100.0%; Score 948; DB 21; 100.0%; Pred. No. 4.8e-89; tive 0; Mismatches 0; Conservative Local Similarity nes 170; Conserv Query Match Best Loca Matches

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ò g CATVTENATGDLATSRNAADSSVPSAPRRQDSEDHSSDMFNYEEYCTANAVTGPCRASFP 120 61 g δ

RWYFDVERNSCNNFIYGGCRGNKNSYRSEEACMLRCFRQQENPPLPLGSK 139 121 óλ

AAW30042 standard; Protein; 213 RESULT 8 AAW30042 DXXXD

AAW30042;

20-APR-1998 (first entry)

cerebral or subsequence of provent brain and spinar condemed. Inflammation, infection or granulomatosis, multiple sclerosis, ischaemia, perioperative blood loss, sepsis, shock, fibrosis, blood coagulation diseases, polytrama, stroke, cerebral or subarachnoid haemorrhage and gastric or cervical cancer and prevent metastasis. It is particularly useful for reducing blood loss during surgery, and can also be used to treat other cancer, arthritis, aneamia, non-insulin dependent diabetes, influenza and similar viral infections, acute pancreatitis and gout, and prevent pre-term labour. It has similar properties to aprotinin, but is less highly charged so should be less immunogenic and less likely to damage the kidneys. Manipulation of the bikunin sequence may allow the inhibitory profile to be allered. It also reduces or eliminates the need for whole donor blood or blood products during surgery, thereby reducing the risk of infection and other adverse side effects, as well as reducing The present sequence is a human placental bikunin, which inhibits, e.g. trypsin, kallikrein, plasmin and factor XIIa. Bikunin can be used to treat or prevent brain and spinal cord Inflammation; infection; granulomatosis; multiple sclerosis; ischaemia; perioperative blood loss; sepsis; shock; fibrosis; blood coagulation disease; polytrauma; stroke; haemorrhage; gastric cancer; cervical cancer; medastasis; blood loss. New human placental bikunin - used to inhibit kallikrein, tetc. in treatment of oedema, multiple sclerosis, fibrosis, perioperative blood loss Tamburini plasmin; factor XIIa; treatment; prevention; oedema; DK, Muller Delaria KA, Marlor CW, Claim 1; Page 65; 110pp; English. 96US-0725251. 96US-0013106. 96US-0019793. 97WO-US03894 WPI; 1997-470876/43. (FARB ) BAYER CORP. 213 AA; WO9733996-A2 10-MAR-1997; 04-OCT-1996; 14-JUN-1996; 11-MAR-1996; 18-SEP-1997 Sequence Davis G, Homo 

61 CATVTENATGDLATSRNAADSSVPSAPRRQDSEDHSSDMFNYEEYCTANAVTGPCRASFP 120 CATVTENATGDLATSRNAADSSVPSAPRRQDSEDHSSDMFNYEEYCTANAVTGPCRASFP 120 Gaps 9 1 ADRERSIHDFCLVSKVVGRCRASMPRWWYNVTDGSCQLFVYGGCDGNSNNYLTKEECLKK 60 1 ADRERSIHDFCLVSKVVGRCRASMPRWWYNVTDGSCQLFVYGGCDGNSNNYLTKEECLKK ; 0 Length 213; Indels RWYFDVERNSCNNFIYGGCRGNKNSYRSEEACMLRCFRQQENPPLPLGSK 100.0%; Score 948; DB 18; ilarity 100.0%; Pred. No. 5.3e-89; Conservative 0; Mismatches 0; Query Match Best Local Similarity Matches 170; Conserv 61 121

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121

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RESULT 9

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                                                                                                                                                        Human; mucocillary dysfunction; mucus; sputum; chronic obstructive lung disease; chronic bronchitis; CB; Bronchiectasis; BE; asthma; cystic fibrosis; CF; bacterial infection; placental bikunin; Kunitz-type serine protease inhibitor; chronic sinusitis; glue ear.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Mucociliary dysfunction is the inability of ciliated epithelium to clear mucus and sputum in lung airways. Mucociliary dysfunction is a serious complication of chronic obstructive lung diseases such as Chronic Bronchitis (CB), Bronchiectasis (BE), asthma and Cystic Fibrosis (CF). In addition, patients suffering from mucociliary dysfunction are susceptible to secondary bacterial infections. The present sequence is a fragment of human placental bikunin. Human placental bikunin is a kunitz-type serine protease inhibitor protein, which can stimulate the rate of mucociliary clearance of mucus and sputum in lung airways. Therefore, the present protein fragment may be used for treating lung diseases such as CF, CB, BE, and chronic sinusitis and glue ear which are caused by retention and accumulation of mucus.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Stimulating mucociliary clearance rate of mucus and sputum in lung airways for treating lung diseases such as cystic fibrosis and bronchitis involves administering a Kunitz-type serine protease inhibitor -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Note: the present sequence is defined as SEQ ID 46 in the sequence listing. However, in figure 4E of the specification, SEQ ID 46 is clearly shown as a nucleotide sequence. Therefore, the nucleotide sequence has been described in AAA70393.
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Pred. No. 5.3e-89;
Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Taylor WJA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Disclosure; Page 162; 173pp; English
                                                                                                                         Human placental bikunin protein # 2.
                AAB14184 standard; protein; 213 AA.
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                                                                                                                                                                                                                                                                                                                                                                                          98US-0218913.
99US-0441966.
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                                                                                     (first entry)
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nes 170; Conserv
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                                                                                                                                                                                                                                                    Homo sapiens.
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17-NOV-1999;
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                                                    AAB14184;
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Matches
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Therefore, the present protein fragment may be used for treating lung diseases such as CF, CB, BE, and chronic sinusitis and glue ear which are caused by retention and accumulation of mucus.
                                                                                                                               Human; mucociliary dysfunction; mucus; sputum; cbs. Bronchiectasis; chronic obstructive lung disease; chronic bronchitis; CB; Bronchiectasis; BE; asthma; cystic fibrosis; CF; bacterial infection; placental bikunin; Kunitz-type serime protease inhibitor; chronic sinusitis; glue ear.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Mucociliary dysfunction is the inability of ciliated epithelium to clea mucus and sputum in lung airways. Mucociliary dysfunction is a serious complication of chronic obstructive lung diseases such as chronic Bronchitis (CB), Bronchiectasis (BE), asthma and Cystic Fibrosis (CF). In addition, patients suffering from mucociliary dysfunction are susceptible to secondary bacterial infections. The present sequence is fragment of human placental bikunin. Human placental bikunin is a kunitz-type serine protease inhibitor protein, which can stimulate the rate of mucociliary clearance of mucus and sputum in lung airways.
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                                                                                                 Human placental bikunin protein fragment # 15.
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AAB14200 standard; protein; 213 AA
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                                                                                                                                                                                                                                                                                                                                                                                                                                        Newton BB,
                                                                                                                                                                                                                                                                                                                                                    98US-0218913.
99US-0441966.
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                                                                (first entry)
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Best Local Similarity
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                                 AAB14200;
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CATVTENATGDLATSRNAADSSVPSAPRRQDSEDHSSDMFNYEEYCTANAVTGPCRASFP 120

RWYFDVERNSCNNFIYGGCRGNKNSYRSEEACMLRCFRQQENPPLPLGSK 170 

121 121 AA.

(first entry)

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Human; mucociliary dysfunction; mucus; sputum; cB; Bronchiectasis; chronic obstructive lung disease; chronic bronchitis; CB; Bronchiectasis; BE; asthma; cystic fibrosis; CF; bacterial infection; placental bikunin; Kunitz-type serine protease inhibitor; chronic sinusitis; glue ear.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Stimulating mucociliary clearance rate of mucus and sputum in lung airways for treating lung diseases such as cystic fibrosis and bronchitis involves administering a Kunitz-type serine protease
                                                                                                                                                                                                                                                                                                      Human placental bikunin protein # 4.
                                                                                                                                                                                   AAB14186 standard; protein; 225
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                                                                                                                                             RESULT 12
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                                                                                                                                                                                               Human; placental bikunin; inhibition; trypsin; kallikrein; plasmin; factor XIIa; treatment; prevention; oedema; inflammation; infection; granulomatosis; multiple sclerosis; ischaemia; perioperative blood loss; sepsis; shock; fibrosis; blood coaquiation disease; polytrauma; stroke; haemorrhage; gastric cancer; cervical cancer; metastasis; blood loss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Length 225;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              New human placental bikunin - used to inhibit kallikrein, tetc. in treatment of oedema, multiple sclerosis, fibrosis,
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Pred. No. 5.7e-89;
Mismatches 0;
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                                     AAW30046 standard; Protein; 225 AA.
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96US-0013106.
96US-0019793.
                                                                                                                     (first entry)
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                                                                                                                                                           Human placental bikunin.
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14-JUN-1996;
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RESULT 11
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Taylor WJA;

Newton BB,

Poll CT,

98US-0218913 99US-0441966 99WO-GB04381

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Mucociliary dysfunction is the inability of ciliated epithelium to clear mucus and sputum in lung airways. Mucociliary dysfunction is a serious complication of chronic obstructive lung diseases such as Chronic CE Tronic obstruction and Cystic Fibrosis (CF). In addition, patients suffering from mucociliary dysfunction are susceptible to secondary bacterial infections. The present sequence is a fragment of human placental bikunin. The present sequence is a Kunitz-type serine protease inhibitor protein, which can stimulate the rate of mucociliary clearance of mucus and sputum in lung airways. Therefore, the present protein fragment may be used for treating lung alseases such as CF, CB, BE, and chronic sinusitis and glue ear which are caused by retention and accumulation of mucus.

Note: the present sequence is defined as SED ID 48 in the sequence listing. However, in figure 4F of the specification, SEO ID 48 is clearly shown as a nucleotide sequence. Therefore, the nucleotide sequence Therefore, the nucleotide control of mucus and sequence Therefore, the nucleotide sequence.
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Disclosure; Page 164; 173pp; English.
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Matches 170;
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CATVTENATGDLATSRNAADSSVPSAPRRQDSEDHSSDMFNYEEYCTANAVTGPCRASFP 120

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1 ADRERSIHDFCLVSKVVGRCRASMPRWWYNVTDGSCQLFVYGGCDGNSNNYLTKEECLKK 60

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100.0%;

Best Local Similarity 100. Matches 170; Conservative

Local Similarity

CATVTENATGDLATSRNAADSSVPSAPRRQDSEDHSSDMFNYEEYCTANAVTGPCRASFP 120

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61 CATVTENATGDLATSRNAADSSVPSAPRRQDSEDHSSDMFNYEEYCTANAVTGPCRASFP 120

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Human; mucociliary dysfunction; mucus; sputum;
chronic Obstructive lung disease; chronic bronchitis; CB; Bronchiectasis;
BE; asthma; cystic fibrosis; CF; bacterial infection; placental bikunin;
Kunitz-type serine protease inhibitor; chronic sinusitis; glue ear.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Mucociliary dysfunction is the inability of ciliated epithelium to clear mucus and sputum in lung airways. Mucociliary dysfunction is a serious complication of chronic obstructive lung diseases such as chronic bronchitis (CB), Bronchiectasis (BE), asthma and Cystic Fibrosis (CF). In addition, patients suffering from mucociliary dysfunction are susceptible to secondary bacterial infections. The present sequence is a fragment of human placental bikunin. Human placental bikunin is a kunitz-type serine protease inhibitor protein, which can stimulate the rate of mucociliary clearance of mucus and sputum in lung airways.
Stimulating mucociliary clearance rate of mucus and sputum in lung airways for treating lung diseases such as cystic fibrosis and bronchitis involves administering a Kunitz-type serine protease
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                                                                             RWYFDVERNSCNNFIYGGCRGNKNSYRSEEACMLRCFRQQENPPLPLGSK 170
                                                                                                           100.0%; Score 948; DB 21;
100.0%; Pred. No. 5.7e-89;
iive 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                     Human placental bikunin protein fragment # 16.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Taylor WJA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Claim 13; Pages 88-89; 173pp; English.
                                                                                                                                                                                                                                                                               AAB14201 standard; protein; 225 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Newton BB,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    99WO-GB04381.
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99US-0441966.
                                                                                                                                                                                                                                                                                                                                                                                                (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        WPI; 2000-452127/39.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Poll CT,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           225 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   WO200037099-A2.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        29-JUN-2000
                                                                                                                                                                                                                                                                                                                                       AAB14201;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 inhibitor
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                    61
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The present sequence is a consensus human bikunin, which inhibits, e.g. trypsin, kallikrein, plasmin and factor XIIa.

Bikunin can be used to treat or prevent brain and spinal cord coedema, inflammation, infection or granulomatosis, multiple sclerosis, ischaemia, perioperative blood loss, sepsis, shock, fibrosis, blood coagulation diseases, polytrauma, stroke, cerebral or subarachnoid heamorrhage and gastric or cervical cancer and prevent metastasis. It is particularly useful for cancer and prevent metastasis. It is particularly useful for cancer and prevent metastasis. It is particularly useful for cher cancer, arthritis, anaemia, non-insulin dependent diabetes, influenza and similar viral infections, acute pancreatitis and gout, and prevent pre-term labour. If has similar properties to aprotinin, but is less highly charged so should be less immunogenic and less likely to damage the kidneys. Manipulation
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                New human placental bikunin - used to inhibit kallikrein, trypsin etc. in treatment of oedema, multiple sclerosis, fibrosis, or perioperative blood loss
                                                                                                                                                                                                                                                   plasmin; factor XIIa; treatment; prevention; oedema; inflammation; infection; granulomatosis; multiple sclerosis; ischaemia; perioperative blood loss; sepsis; shock; fibrosis; blood coagulation disease; polytrauma; stroke; haemorrhage; gastric cancer; cervical cancer; metastasis; blood loss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Tamburini PP;
RWYFDVERNSCNNFIYGGCRGNKNSYRSEEACMLRCFRQQENPPLPLGSK 170
                                                                                                                                                                                                                                       consensus bikunin; inhibition; trypsin; kallikrein;
                Muller DK,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 by GAN"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              "encoded by TGA"
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                                                                                                                                                                                                                                                                                                                                                                                  Location/Qualifiers
                                                                                                             AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Disclosure; Fig 3; 110pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Marlor CW,
                                                                                                           AAW30060 standard; Protein; 235
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               "encoded
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96US-0013106.
96US-0019793.
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                                                                                                                                                                        (first entry)
                                                                                                                                                                                                        Human consensus bikunin.
                                                                                                                                                                                                                                                                                                                                                                                                                   'note=
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                                                                                                                                                                                                                                                                                                                                                                                                 Misc-difference 198
                                                                                                                                                                                                                                                                                                                                                                                                                                                              Misc-difference 226
                                                                                                                                                                                                                                                                                                                                                                                                                                 Misc-difference 201
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        11-MAR-1996;
14-JUN-1996;
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                                                                                                                                         AAW30060;
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Gaps

Indels

9

CATVTENATGDLATSRNAADSSVPSAPRRQDSEDHSSDMFNYEEYCTANAVTGPCRASFP 120

61

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1 ADRERSIHDFCLVSKVVGRCRASMPRWWYNVTDGSCQLFVYGGCDGNSNNYLTKEECLKK 60

Conservative

Similarity

Best Local Sim. Matches 170;

1 ADRERSIHDFCLVSKVVGRCRASMPRWWYNVTDGSCQLEVYGGCDGNSNNYLTKEECLKK

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                                                                                                                                                                                                                                                                                                                                                                                                                                                chronic obstructive lung disease; chronic bronchitis; CB; Bronchiectasis; BB; asthma; cystic fibrosis; CF; bacterial infection; placental bikunin; Kunitz-type serine protease inhibitor; chronic sinusitis; glue ear.
                                                                                                                                                                                                61 CATVTENATGDLATSRNAADSSVPSAPRRQDSEDHSSDMFNYEEYCTANAVTGPCRASFP 120
                                                                                                                                                                         78
                                                                                                                                                                                                              of the bikunin sequence may allow the inhibitory profile to be altered. It also reduces or eliminates the need for whole donor blood or blood products during surgery, thereby reducing the risk of infection and other adverse side effects, as well as reducing
                                                                                                                                                1 ADRERSIHDFCLVSKVVGRCRASMPRWWYNVTDGSCQLFVYGGCDGNSNNYLTKEECLKK
                                                                                                                                                               19 ADRERSIHDFCLVSKVVGRCRASMPRWYNVTDGSCQLFVYGGCDGNSNNYLTKEECLKK
                                                                                                  Length 235;
                                                                                                                                                                                                                                                             139 RWYFDVERNSCNNFIYGGCRGNKNSYRSEEACMLRCFRQQENPPLPLGSK 188
                                                                                                                                                                                                                                               RWYFDVERNSCNNFIYGGCRGNKNSYRSEEACMLRCFRQQENPPLPLGSK 170
                                                                                                  DB 18;
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0
                                                                                                Score 948; DB 18
Pred. No. 6e-89;
; Mismatches C
                                                                                                                                                                                                                                                                                                                                                                                                                                    mucociliary dysfunction; mucus; sputum;
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                                                                                              100.0%; Scilarity 100.0%; Pr
Conservative 0;
                                                                                                                                                                                                                                                                                                                                     235
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/note= "Encoded
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                                                                                                                                                                                                                                                                                                                                    AAB14167 standard; Protein;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           99US-0441966
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                                                  the cost of surgery
                                                                                                            Best_Local Similarity
Matches 170; Conserv
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17-NOV-1999;
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                                                                          Sequence
                                                                                                  Query Match
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completed: October 18, 2002, 10:34:47

Job time :

Search

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                                                                                                                                                               Mucociliary dysfunction is the inability of ciliated epithelium to clear mucus and sputum in lung airways. Mucociliary dysfunction is a serious complication of chronic obstructive lung diseases such as Chronic Bronchitis (CB), Bronchiectasis (BE), asthma and Cystic Fibrosis (CF). In addition, patients suffering from mucociliary dysfunction are susceptible to secondary bacterial infections. The present sequence is a human placental bikunin protein fragment. This protein is a Kunitz-type serine protease inhibitor protein, and shall a stimulate the rate of mucociliary clearance of mucus and sputum in lung airways. Therefore, the
                                                                                                                                                                                                                                                                                                                                                                    present sequence may be used for treating lung diseases such as CF, CB, BE, and chronic sinusitis and glue ear which are caused by retention and accumulation of {\tt mucus}.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CATVTENATGDLATSRNAADSSVPSAPRRODSEDHSSDMFNYEEYCTANAVTGPCRASFP 120
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                  Stimulating mucociliary clearance rate of mucus and sputum in lung airways for treating lung diseases such as cystic fibrosis and bronchitis involves administering a Kunitz-type serine protease
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1 ADRERSIHDFCLVSKVVGRCRASMPRWWYNVTDGSCQLFVYGGCDGNSNNYLTKEECLKK
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Length 235;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 100.0%; Score 948; DB 21;
llarity 100.0%; Pred. No. 6e-89;
Conservative 0; Mismatches 0;
                                                                                                                            Disclosure; Fig 3; 173pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                           235 AA;
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                                                                                 inhibitor
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